

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:05:38 ; Search time 232 Seconds
(without alignments)
408.258 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaagca 16

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: N_Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	16	2	AAT18256
2	16	100.0	16	2	AAV14125
3	16	100.0	16	10	ADB68575
4	16	100.0	17	8	ACD55710
5	16	100.0	17	8	ACD53930
6	16	100.0	17	12	ADM59621
7	16	100.0	17	12	ADM60244
8	16	100.0	18	2	AAT71786
9	16	100.0	18	2	AAV14133
10	16	100.0	19	2	AAT71785
11	16	100.0	19	2	AAT71789
12	16	100.0	19	11	ADM00160
13	16	100.0	19	11	ADM00806
14	16	100.0	19	11	ADM00807
15	16	100.0	19	11	ADM00284
16	16	100.0	19	11	ADM00804
17	16	100.0	19	11	ADL9637
18	16	100.0	19	11	ADM00161
19	16	100.0	19	11	ADM00158
20	16	100.0	20	2	AAQ13771

C	21	16	100.0	20	2	AAQ13772	AaQ13772 HBV prime
C	22	16	100.0	20	2	AAQ85970	AaQ85970 Hepatitis
C	23	16	100.0	20	2	AAT70947	AaT70947 HBV pre-g
C	24	16	100.0	21	2	AAQ32909	AaQ32909 Antiviral
C	25	16	100.0	21	2	AAT18255	AaT18255 HBV eps1
C	26	16	100.0	21	2	AAT18253	AaT18253 HBV eps1
C	27	16	100.0	21	2	AAT70936	AaT70936 HBV core
C	28	16	100.0	21	9	ADA13842	Ada13842 Short int
C	29	16	100.0	21	11	ADM00924	Adm00924 Hepatitis
C	30	16	100.0	23	2	AAQ13770	AaQ13770 HBV prime
C	31	16	100.0	23	2	AAT03266	AaT03266 Hepatitis
C	32	16	100.0	23	2	AAQ81424	AaQ81424 HBV hyp1
C	33	16	100.0	23	4	AAQ19005	AaQ19005 Hepatitis
C	34	16	100.0	23	11	ADM00880	Adm00880 Hepatitis
C	35	16	100.0	30	2	AAV29303	AaV29303 Hepatitis
C	36	16	100.0	32	4	AA514628	Aa514628 NASBA mol
C	37	16	100.0	44	2	AAT71784	AaT71784 Hepatitis
C	38	16	100.0	44	2	AAT71783	AaT71783 Hepatitis
C	39	16	100.0	48	3	ABK14698	AbK14698 HBV encap
C	40	16	100.0	48	3	ABK14696	AbK14696 RNA target
C	41	16	100.0	50	2	AAQ81436	AaQ81436 HBV target
C	42	16	100.0	54	3	AA294421	Aa294421 Hepatitis
C	43	16	100.0	61	3	ABK14697	AbK14697 HBV prege
C	44	16	100.0	61	9	ACA62424	AaC62424 Hepatitis
C	45	16	100.0	70	2	AAQ28267	AaQ28267 Sequence
C	46	16	100.0	72	2	AAT58386	AaT58386 Hepatitis
C	47	16	100.0	87	2	AAT05545	AaT05545 Human hep
C	48	16	100.0	87	4	AAQ09094	AaQ09094 Hepatitis
C	49	16	100.0	94	2	AAT73890	AaT73890 Human hep
C	50	16	100.0	94	2	AAT73887	AaT73887 Human hep
C	51	16	100.0	94	2	AAT73889	AaT73889 Human hep
C	52	16	100.0	94	2	AAT73888	AaT73888 Human hep
C	53	16	100.0	114	2	AAQ25403	AaQ25403 Sequence
C	54	16	100.0	129	4	AAQ09093	AaQ09093 Hepatitis
C	55	16	100.0	137	2	AAK34316	AaK34316 Fragment
C	56	16	100.0	291	2	AAQ25406	AaQ25406 Sequence
C	57	16	100.0	299	13	ADP79740	AdP79740 Hepatitis
C	58	16	100.0	390	2	AAQ25411	AaQ25411 Sequence
C	59	16	100.0	534	2	AAQ25399	AaQ25399 Sequence
C	60	16	100.0	534	2	AAQ25400	AaQ25400 HBV core
C	61	16	100.0	534	2	AAT05543	AaT05543 Human hep
C	62	16	100.0	560	10	ABT23617	AbT23617 Scab11st
C	63	16	100.0	560	10	ABT23618	AbT23618 Scab11st
C	64	16	100.0	560	12	ADN00634	AdN00634 Hepatitis
C	65	16	100.0	588	2	AAQ25640	AaQ25640 Sequence
C	66	16	100.0	639	6	AAQ27422	AaQ27422 Hepatitis
C	67	16	100.0	639	6	AAQ31509	AaQ31509 Hepatitis
C	68	16	100.0	646	12	ADL56756	AdL56756 HBV prece
C	69	16	100.0	655	2	AAQ47014	AaQ47014 HBV (adv)
C	70	16	100.0	655	2	AAT35649	AaT35649 Precore/c
C	71	16	100.0	655	4	AAH77569	AaH77569 HBV genot
C	72	16	100.0	655	4	AAH77568	AaH77568 HBV genot
C	73	16	100.0	655	4	AAH77574	AaH77574 HBV genot
C	74	16	100.0	655	4	AAH77573	AaH77573 HBV genot
C	75	16	100.0	655	4	AAH77570	AaH77570 HBV genot
C	76	16	100.0	655	4	AAH77571	AaH77571 HBV genot
C	77	16	100.0	655	4	AAQ21244	AaQ21244 Hepatitis
C	78	16	100.0	655	9	ABX80077	AbX80077 Hepatitis
C	79	16	100.0	655	10	ABX96938	AbX96938 Hepatitis
C	80	16	100.0	660	1	AAQ1081	AaQ1081 DNA beque
C	81	16	100.0	663	3	AAV11734	AaV11734 HBV fusio
C	82	16	100.0	664	4	AAH77572	AaH77572 HBV genot
C	83	16	100.0	669	12	ADQ07220	AdQ07220 Hepatitis
C	84	16	100.0	673	4	AAQ09092	AaQ09092 Hepatitis
C	85	16	100.0	675	4	AAH77563	AaH77563 HBV prece
C	86	16	100.0	681	4	AAH77566	AaH77566 HBV genot
C	87	16	100.0	681	4	AAH77567	AaH77567 HBV genot
C	88	16	100.0	750	1	AAQ80943	AaQ80943 HBV core
C	89	16	100.0	909	6	AAH77169	AaH77169 Regulator
C	90	16	100.0	1334	2	AAV82691	AaV82691 Fulminant
C	91	16	100.0	1395	2	AAV82688	AaV82688 Fulminant
C	92	16	100.0	1400	2	AAV82687	AaV82687 Fulminant
C	93	16	100.0	1445	2	AAV82692	AaV82692 Fulminant

C 94	16	100.0	1445	2	AAV82685	AAV82685 Fulminant	C 167	15	93.8	30	6	ABT50306	ABT50306 Hepatitis
C 95	16	100.0	1445	2	AAV82690	AAV82690 Fulminant	C 168	15	93.8	644	3	AAFL4461	AAFL4461 Aspergill
C 96	16	100.0	1445	2	AAV82684	AAV82684 Fulminant	C 96	15	696	9	ADA50189	ADA50189 Human cDN	
C 97	16	100.0	1500	2	AAV82695	AAV82695 Fulminant	C 169	15	93.8	866	9	ABT19286	ABT19286 Aspergill
C 98	16	100.0	1500	2	AAV82683	AAV82683 Fulminant	C 170	15	93.8	864	8	ABT19286	ABT19286 Aspergill
C 99	16	100.0	1500	2	AAV82694	AAV82694 Fulminant	C 171	15	93.8	1041	8	ABT21106	ABT21106 Aspergill
C 100	16	100.0	1500	2	AAV82697	AAV82697 Fulminant	C 172	15	93.8	1041	8	ABT18692	ABT18692 Aspergill
C 101	16	100.0	1500	2	AAV82686	AAV82686 Fulminant	C 173	15	93.8	1041	8	ABT20508	ABT20508 Aspergill
C 102	16	100.0	1500	2	AAV82706	AAV82706 Fulminant	C 174	15	93.8	1591	5	AA566799	AA566799 DNA encod
C 103	16	100.0	1500	2	AAV82689	AAV82689 Fulminant	C 175	15	93.8	1591	5	AA566799	AA566799 DNA encod
C 104	16	100.0	1500	2	AAV82693	AAV82693 Fulminant	C 176	15	93.8	3041	8	ABT19912	ABT19912 DNA encod
C 105	16	100.0	1503	2	AAV82696	AAV82696 Fulminant	C 177	15	93.8	3041	8	ABT18098	ABT18098 Aspergill
C 106	16	100.0	1841	6	ABQ70492	ABQ70492 Listeria	C 178	15	93.8	3215	6	ABLS5204	ABLS5204 HBV subty
C 107	16	100.0	1977	12	ADJ53703	ADJ53703 RNA pseud	C 179	15	93.8	4682	12	AD086465	AD086465 Human tss
C 108	16	100.0	2342	1	AAV93072	AAV93072 Sequence	C 180	15	93.8	4682	13	ACN39455	ACN39455 Tumour-as
C 109	16	100.0	2743	1	AAV00003	AAV00003 Sequence	C 181	15	93.8	4692	10	AD573109	AD573109 Human cel
C 110	16	100.0	2743	1	AAV00003	AAV00003 Sequence	C 182	15	93.8	4692	13	AD573109	AD573109 Human cel
C 111	16	100.0	3180	4	AAH42375	AAH42375 Recombina	C 183	15	93.8	4896	4	AA159468	AA159468 Human pol
C 112	16	100.0	3182	6	AAH42375	AAH42375 Recombina	C 184	15	93.8	4896	4	AA159468	AA159468 Human pol
C 113	16	100.0	3182	6	AAH42375	AAH42375 Recombina	C 185	15	93.8	4896	4	AA159468	AA159468 Human pol
C 114	16	100.0	3182	6	AAH42375	AAH42375 Recombina	C 186	15	93.8	4896	4	AA159468	AA159468 Human pol
C 115	16	100.0	3182	6	AAH42375	AAH42375 Recombina	C 187	15	93.8	4896	4	AA159468	AA159468 Human pol
C 116	16	100.0	3188	1	AAH40244	AAH40244 DNA cong	C 188	15	93.8	6663	3	AD748447	AD748447 Human ORF
C 117	16	100.0	3188	12	ADN16973	ADN16973 Hepatitis	C 189	15	93.8	48133	11	ACN44860	ACN44860 Mouse ge
C 118	16	100.0	3188	12	ADN16973	ADN16973 Hepatitis	C 190	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 119	16	100.0	3192	2	AAV088222	AAV088222 X region	C 191	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 120	16	100.0	3200	1	AAV088222	AAV088222 X region	C 192	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 121	16	100.0	3200	1	AAV088222	AAV088222 X region	C 193	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 122	16	100.0	3207	2	AAV088222	AAV088222 X region	C 194	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 123	16	100.0	3214	1	AAV088222	AAV088222 X region	C 195	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 124	16	100.0	3214	1	AAV088222	AAV088222 X region	C 196	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 125	16	100.0	3215	3	AAZ29453	AAZ29453 Mutant he	C 197	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 126	16	100.0	3215	3	AAZ29453	AAZ29453 Mutant he	C 198	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 127	16	100.0	3215	3	AAZ29453	AAZ29453 Mutant he	C 199	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 128	16	100.0	3215	3	AAZ29453	AAZ29453 Mutant he	C 200	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 129	16	100.0	3221	12	ADM16810	ADM16810 Hepatitis	C 201	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 130	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 202	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 131	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 203	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 132	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 204	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 133	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 205	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 134	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 206	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 135	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 207	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 136	16	100.0	3221	4	AAH42374	AAH42374 Nucleotid	C 208	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 137	16	100.0	3248	4	AAH77562	AAH77562 HBV genot	C 209	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 138	16	100.0	3248	4	AAH77562	AAH77562 HBV genot	C 210	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 139	16	100.0	3835	2	AAQ05378	AAQ05378 Sequence	C 211	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 140	16	100.0	4084	4	AAH42374	AAH42374 Nucleotid	C 212	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 141	16	100.0	4421	2	AAH42374	AAH42374 Nucleotid	C 213	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 142	16	100.0	4421	2	AAH42374	AAH42374 Nucleotid	C 214	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 143	16	100.0	4839	4	ABL08429	ABL08429 Hepatitis	C 215	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 144	16	100.0	5037	12	ADJ27202	ADJ27202 Fruityly	C 216	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 145	16	100.0	5618	2	AAQ88310	AAQ88310 Plasmid p	C 217	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 146	16	100.0	5639	2	AAH77562	AAH77562 HBV genot	C 218	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 147	16	100.0	5676	13	ADJ27202	ADJ27202 Fruityly	C 219	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 148	16	100.0	6371	2	AAZ23282	AAZ23282 DNA seque	C 220	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 149	16	100.0	6371	2	AAZ23282	AAZ23282 DNA seque	C 221	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 150	16	100.0	6942	4	AAH42374	AAH42374 Nucleotid	C 222	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 151	16	100.0	7085	4	AAH42374	AAH42374 Nucleotid	C 223	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 152	16	100.0	7991	6	AAH42374	AAH42374 Nucleotid	C 224	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 153	16	100.0	8007	6	AAH42374	AAH42374 Nucleotid	C 225	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 154	16	100.0	8717	6	AAH42374	AAH42374 Nucleotid	C 226	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 155	16	100.0	9325	2	AAZ23282	AAZ23282 DNA seque	C 227	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 156	16	100.0	9325	2	AAZ23282	AAZ23282 DNA seque	C 228	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 157	16	100.0	9534	2	AAZ23282	AAZ23282 DNA seque	C 229	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 158	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 230	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 159	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 231	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 160	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 232	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 161	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 233	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 162	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 234	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 163	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 235	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 164	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 236	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 165	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 237	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 166	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 238	15	93.8	53021	11	ACN44945	ACN44945 Human gen
C 167	16	100.0	9542	2	AAZ23282	AAZ23282 DNA seque	C 239	15	93.8	53021	11	ACN44945	ACN44945 Human gen

C 240	14	87.5	2233	4	ABL17591	ABL17591 Drosophila	C 313	13	81.2	23	11	ADM00889	Adm00889 Hepatitis
241	14	87.5	3026	13	ADQ86001	Adq86001 Human tum	C 314	13	81.2	27	2	AAT05554	Aat05554 Human hep
242	14	87.5	3026	13	ADQ87475	Adq87475 Human tum	C 315	13	81.2	30	2	AAO74959	Aao74959 Hepatitis
243	14	87.5	3034	6	ABK83882	Abk83882 Human CDN	C 316	13	81.2	30	2	AAO74960	Aao74960 Hepatitis
244	14	87.5	3034	6	ABZ71983	Abz71983 Human pho	C 317	13	81.2	34	2	AAO47022	Aao47022 HBV preco
C 245	14	87.5	3150	4	ABL18734	AbL18734 Drosophila	C 318	13	81.2	34	2	AAQ86218	Aaq86218 HBV adw b
C 246	14	87.5	3274	4	ABL18736	AbL18736 Drosophila	C 319	13	81.2	34	2	AAT35660	Aat35660 Primer #3
247	14	87.5	3452	12	ADM79336	Adm79336 Mouse 1ym	C 320	13	81.2	34	2	AAT31174	Aat31174 XhoI site
248	14	87.5	3454	6	AAD41009	Aad41009 Mouse P13	C 321	13	81.2	34	2	AAV42449	Aav42449 PCR prime
249	14	87.5	3454	6	ABK72319	Abk72319 DNA encod	C 322	13	81.2	34	2	AAV62028	Aav62028 Sense PCR
250	14	87.5	3454	6	ABK72292	Abk72292 Lymphona	C 323	13	81.2	34	2	AAV30014	Aav30014 PCR prime
251	14	87.5	3454	6	ABSS4198	Abss4198 Mouse CDN	C 324	13	81.2	34	2	AAV70769	Aav70769 PCR prime
252	14	87.5	3454	6	ADA02928	Ada02928 Mouse P13	C 325	13	81.2	34	3	AAZ92993	Aaz92993 HBV core
253	14	87.5	3454	10	ADB72666	Adb72666 Mouse P13	C 326	13	81.2	34	3	AAZ92866	Aaz92866 HBV core
254	14	87.5	3454	10	ADC85408	Adc85408 Mouse P13	C 327	13	81.2	34	4	AAZ21195	Aaz21195 Sense PCR
255	14	87.5	3454	12	ADM79337	Adm79337 Mouse 1ym	C 328	13	81.2	34	6	AAI38873	Aai38873 Alphaviru
256	14	87.5	3454	12	ADM74523	Adm74523 Murine 1ym	C 329	13	81.2	34	6	ABK46339	Abk46339 HBV core
257	14	87.5	3454	12	ADQ60051	Adq60051 CSH signa	C 330	13	81.2	34	9	ABK80029	Abk80029 Hepatitis
258	14	87.5	3523	6	ABQ54610	Abq54610 Human ova	C 331	13	81.2	34	10	ABX96890	Abx96890 Hepatitis
259	14	87.5	3633	2	AAT97611	Aat97611 Mouse E2A	C 332	13	81.2	34	12	ADI30446	Adi30446 HBV core
260	14	87.5	3728	2	AAQ58708	Aaq58708 Mouse OSF	C 333	13	81.2	34	12	ADL56744	Adl56744 HBV core
261	14	87.5	3854	2	AAT97610	Aat97610 Human E2A	C 334	13	81.2	34	12	ADQ14005	Adq14005 Burkaryot
262	14	87.5	3872	10	ADER9063	Der9063 Human pro	C 335	13	81.2	80	12	ADM96072	Adm96072 Rat antiB
263	14	87.5	3914	12	ADQ86121	Adq86121 Human tum	C 336	13	81.2	94	2	AAT73892	Aat73892 Human hep
264	14	87.5	3914	13	ACN38620	Acn38620 Tumour-48	C 337	13	81.2	94	2	AAT73891	Aat73891 Human hep
265	14	87.5	3922	9	ACH03928	Ach03928 Human CDN	C 338	13	81.2	141	2	AAT69055	Aat69055 Hepatitis
266	14	87.5	3935	8	ABZ34770	Abz34770 Coding se	C 339	13	81.2	207	5	AAH67687	Aah67687 C glutami
267	14	87.5	3935	8	ACC50076	Acc50076 Breast ca	C 340	13	81.2	228	12	ACH93965	Ach93965 Human gen
268	14	87.5	3935	10	ADP90653	Adp90653 Human hep	C 341	13	81.2	231	8	ACA01159	Acca01159 C. glutam
269	14	87.5	4025	10	ADER9067	Der9067 Human pro	C 342	13	81.2	231	12	ADQ21864	Adq21864 Human bof
270	14	87.5	4125	13	ADRA4022	Adra4022 Human col	C 343	13	81.2	240	2	AAH86378	Aah86378 Human sin
271	14	87.5	4233	13	ABL17590	AbL17590 Drosophila	C 344	13	81.2	240	2	AAH86380	Aah86380 Human sin
272	14	87.5	4236	8	ACA39046	AcA39046 Prokaryot	C 345	13	81.2	240	4	AAI23709	Aai23709 Probe #13
273	14	87.5	4269	12	ADL03415	AdL03415 DNA encod	C 346	13	81.2	240	4	ABA68824	AbA68824 Human floe
274	14	87.5	4483	4	ABL07558	AbL07558 Drosophila	C 347	13	81.2	240	4	AAI49022	Aai49022 Probe #17
C 275	14	87.5	5513	3	AAC63529	Aac63529 SLIT prot	C 348	13	81.2	240	4	ABA50851	AbA50851 Human bre
C 276	14	87.5	6391	13	ADQ85331	Adq85331 Human tum	C 349	13	81.2	240	4	ABA55777	AbA55777 Probe #14
277	14	87.5	6502	10	ADG32776	Adg32776 Human DNA	C 350	13	81.2	240	4	AAK42945	Aak42945 Human bon
278	14	87.5	6627	5	AAH86211	Aah86211 DNA encod	C 351	13	81.2	240	4	AAK17160	Aak17160 Human bra
279	14	87.5	6781	13	ACNA42918	Acna42918 Human dia	C 352	13	81.2	240	4	ABSA42577	AbSA42577 Human liv
280	14	87.5	6997	13	ACNA42917	Acna42917 Human dia	C 353	13	81.2	240	5	AAI09326	Aai09326 Probe #93
281	14	87.5	7697	9	ACD28255	AcD28255 Mouse sol	C 354	13	81.2	240	6	ABSI17007	AbSI17007 Human gen
282	14	87.5	10558	4	ABL02846	AbL02846 Drosophila	C 355	13	81.2	243	10	ADH84063	Adh84063 Enterococ
283	14	87.5	13104	4	AAQ46852	Aaq46852 Clone of	C 356	13	81.2	282	13	ADR91549	Adr91549 Novel S.
C 284	14	87.5	16161	6	AAJ36071	Aaj36071 Human adi	C 357	13	81.2	289	13	ADR29684	Adr29684 Mouse gen
285	14	87.5	18737	4	ABL07492	AbL07492 Drosophila	C 358	13	81.2	300	2	AAZ14607	Aaz14607 Human gen
286	14	87.5	18737	4	ABL07530	AbL07530 Drosophila	C 359	13	81.2	308	13	ADR93088	Adr93088 Novel S.
287	14	87.5	31063	4	AAF28533	Aaf28533 Genomic f	C 360	13	81.2	339	12	ADQ18067	Adq18067 Human bof
C 288	14	87.5	43229	11	ACNA4192	Acna4192 Mouse gen	C 361	13	81.2	343	8	ABX42722	Abx42722 Bovine ES
289	14	87.5	53601	12	ADQ97749	Adq97749 Human can	C 362	13	81.2	365	9	ABZ37683	Abz37683 Porcine 5
290	14	87.5	80268	13	ABD32951	Abd32951 Mouse can	C 363	13	81.2	394	9	ACH25666	Ach25666 Human adu
291	14	87.5	80578	9	AAH44800	Aah44800 Human GPC	C 364	13	81.2	396	4	AAI81388	Aai81388 Human pol
292	14	87.5	92726	9	ADA02927	Ada02927 Mouse P13	C 365	13	81.2	399	10	ADR81376	Adr81376 Leukaemia
293	14	87.5	92726	10	ADB72665	AdB72665 Mouse P13	C 366	13	81.2	401	9	AAI60864	Aai60864 Human CYP
294	14	87.5	92726	10	ADC85407	AdC85407 Mouse P13	C 367	13	81.2	416	5	ABV62019	Abv62019 Human pro
295	14	87.5	92726	12	ADM74522	Adm74522 Murine ca	C 368	13	81.2	416	5	ABV62117	Abv62117 Human pro
C 296	14	87.5	100137	9	ADQ97643	AdQ97643 Human can	C 369	13	81.2	416	5	ABV61984	Abv61984 Human pro
C 297	14	87.5	110000	12	ADQ87053	AdQ87053 Human can	C 370	13	81.2	420	3	ADR57131	Adr57131 Urogenita
C 298	14	87.5	122779	12	ADQ87053	AdQ87053 Mouse can	C 371	13	81.2	420	3	ADR57131	Adr57131 Urogenita
299	14	87.5	129017	12	ADP84158	Adp84158 Human AST	C 372	13	81.2	421	12	ADQ80746	Adq80746 Porcine e
C 300	14	87.5	162450	3	AAZ86967	Aaz86967 Retinobla	C 373	13	81.2	427	6	ABL82633	AbL82633 Human ova
C 301	13	81.2	15	8	ACD56186	AcD56186 HBV enzym	C 374	13	81.2	438	9	ACL20721	ACL20721 DNA clone
C 302	13	81.2	15	12	ADM63883	Adm63883 Hepatitis	C 375	13	81.2	440	13	ADQ53724	AdQ53724 Novel can
C 303	13	81.2	16	8	AAT18258	Aat18258 HBV epsil	C 376	13	81.2	444	6	ABR9498	AbR9498 Human CYP
C 304	13	81.2	17	8	ACD53523	AcD53523 HBV inozy	C 377	13	81.2	449	4	AAI14509	Aai14509 Probe #44
C 305	13	81.2	17	8	ACD53531	AcD53531 HBV ziny	C 378	13	81.2	449	4	ABA56240	AbA56240 Human E06
C 306	13	81.2	17	12	ADM59622	Adm59622 Hepatitis	C 379	13	81.2	449	4	AAI15884	Aai15884 Probe #45
C 307	13	81.2	17	12	ADM59016	Adm59016 Hepatitis	C 380	13	81.2	449	4	ABA45731	AbA45731 Human bre
C 308	13	81.2	19	11	ADM00283	Adm00283 Hepatitis	C 381	13	81.2	449	4	ABA25880	AbA25880 Probe #43
C 309	13	81.2	19	11	ADL99636	Adl99636 Hepatitis	C 382	13	81.2	449	4	AAK29919	Aak29919 Human bon
C 310	13	81.2	20	2	AAQ81425	Aaq81425 HBV hybr	C 383	13	81.2	449	4	AAK04423	Aak04423 Human bra
C 311	13	81.2	21	2	AAT18257	Aat18257 HBV epsil	C 384	13	81.2	449	4	ABSS29568	Abss29568 Human liv
C 312	13	81.2	21	11	ADM00999	Adm00999 Hepatitis	C 385	13	81.2	449	5	AAI04334	Aai04334 Probe #43

386	13	81.2	449	6	ABSO4487	Abp04487 Human gen	C 459	13	81.2	628	9	ACL20732	ACL20732 DNA clone
387	13	81.2	456	9	ACH35437	ACH35437 Human end	C 460	13	81.2	629	9	ACL20743	ACL20743 DNA clone
C 388	13	81.2	454	10	ADK61537	ADK61537 Ovarian c	C 461	13	81.2	634	9	ACL20769	ACL20769 DNA clone
389	13	81.2	463	10	ABZ84631	ABZ84631 Toxicrolog	C 462	13	81.2	634	9	ACL20773	ACL20773 DNA clone
390	13	81.2	464	4	AA111903	AA111903 Probe #18	C 463	13	81.2	637	9	ACL20708	ACL20708 DNA clone
391	13	81.2	464	4	ABAB3606	ABAB3606 Human foe	C 464	13	81.2	640	9	ACL20765	ACL20765 DNA clone
392	13	81.2	464	4	AA133233	AA133233 Probe #19	C 465	13	81.2	642	8	ACAA9691	ACAA9691 Prokaryot
393	13	81.2	464	4	ABAB3361	ABAB3361 Probe #18	C 466	13	81.2	644	9	ACL20697	ACL20697 DNA clone
394	13	81.2	464	4	AAK27329	AAK27329 Human Don	C 467	13	81.2	645	9	ACL20698	ACL20698 DNA clone
395	13	81.2	464	4	AAK01872	AAK01872 Human bra	C 468	13	81.2	647	4	AAK63140	AAK63140 Human imm
396	13	81.2	464	4	ABG26903	ABG26903 Human bra	C 469	13	81.2	648	9	ACL20758	ACL20758 DNA clone
C 398	13	81.2	469	5	ABSO1849	ABSO1849 Human gen	C 470	13	81.2	653	2	AAV52491	AAV52491 DNA clone
399	13	81.2	478	9	ACH41721	ACH41721 Human pro	C 471	13	81.2	654	9	ACL20738	ACL20738 DNA clone
400	13	81.2	478	9	ACH13859	ACH13859 Human foe	C 472	13	81.2	658	9	ACL20745	ACL20745 DNA clone
C 401	13	81.2	485	9	ACL20701	ACL20701 Human adu	C 473	13	81.2	659	3	AAAS1795	AAAS1795 DNA clone
C 402	13	81.2	487	13	ACNS1896	ACNS1896 Cotton an	C 474	13	81.2	660	9	ACL20699	ACL20699 DNA clone
C 403	13	81.2	492	9	ACL20696	ACL20696 DNA clone	C 475	13	81.2	664	9	ACL20760	ACL20760 DNA clone
C 404	13	81.2	492	9	ACL20695	ACL20695 DNA clone	C 476	13	81.2	671	9	ACL20768	ACL20768 DNA clone
C 405	13	81.2	493	10	ADBS5993	ADBS5993 Toxicity-	C 477	13	81.2	674	9	ACL20719	ACL20719 DNA clone
C 406	13	81.2	498	9	ACH24092	ACH24092 Human adu	C 478	13	81.2	681	10	ABX07776	ABX07776 S. pneumo
C 407	13	81.2	501	9	ACH41422	ACH41422 Human foe	C 479	13	81.2	682	9	ACL20766	ACL20766 DNA clone
C 408	13	81.2	503	9	ACH41422	ACH41422 Human foe	C 480	13	81.2	687	9	ACL20714	ACL20714 DNA clone
C 409	13	81.2	505	9	ACL20720	ACL20720 DNA clone	C 481	13	81.2	687	9	ACL20694	ACL20694 DNA clone
C 410	13	81.2	509	9	ACL20716	ACL20716 DNA clone	C 482	13	81.2	688	9	ACL20715	ACL20715 DNA clone
C 411	13	81.2	519	13	ACNS8104	ACNS8104 Cotton gy	C 483	13	81.2	690	9	ACL20723	ACL20723 DNA clone
C 412	13	81.2	524	9	ACL20733	ACL20733 DNA clone	C 484	13	81.2	692	9	ACL20706	ACL20706 DNA clone
C 413	13	81.2	526	13	ACNS8123	ACNS8123 Cotton gy	C 485	13	81.2	694	9	ACL20729	ACL20729 DNA clone
C 414	13	81.2	536	9	ACL20750	ACL20750 DNA clone	C 486	13	81.2	700	9	ACL20718	ACL20718 DNA clone
C 415	13	81.2	537	12	ACH80265	ACH80265 Human gen	C 487	13	81.2	707	9	ACL20705	ACL20705 DNA clone
C 416	13	81.2	539	9	AAPO9493	AAPO9493 Fuesarium	C 488	13	81.2	709	9	ACL20726	ACL20726 DNA clone
C 417	13	81.2	542	9	ACL20702	ACL20702 DNA clone	C 489	13	81.2	718	10	ADFB82745	ADFB82745 DNA clone
C 418	13	81.2	542	9	ACL20746	ACL20746 DNA clone	C 490	13	81.2	722	9	ACL20704	ACL20704 DNA clone
C 419	13	81.2	542	9	ACL20761	ACL20761 DNA clone	C 491	13	81.2	725	4	AAH34565	AAH34565 Human col
C 420	13	81.2	543	13	ADBS34562	ADBS34562 POSH prot	C 492	13	81.2	729	12	ADU43417	ADU43417 Plant cDN
C 421	13	81.2	545	9	ACL20749	ACL20749 DNA clone	C 493	13	81.2	735	12	ADU43418	ADU43418 Plant cDN
C 422	13	81.2	547	9	ACL20707	ACL20707 DNA clone	C 494	13	81.2	741	10	ADU34290	ADU34290 Mouse mit
C 423	13	81.2	553	9	ACL20710	ACL20710 DNA clone	C 495	13	81.2	762	5	AAH70070	AAH70070 DNA encod
C 424	13	81.2	553	9	ACL20764	ACL20764 DNA clone	C 496	13	81.2	786	4	AAH16187	AAH16187 Human bre
C 425	13	81.2	553	9	ACL20727	ACL20727 DNA clone	C 497	13	81.2	886	4	AAH25030	AAH25030 Human bre
C 426	13	81.2	554	9	ACL20735	ACL20735 DNA clone	C 498	13	81.2	912	6	AAH66472	AAH66472 Streptoco
C 427	13	81.2	558	9	ACL20736	ACL20736 DNA clone	C 499	13	81.2	912	6	AAH66472	AAH66472 Streptoco
C 428	13	81.2	558	9	ACL20752	ACL20752 DNA clone	C 500	13	81.2	912	11	ADU12093	ADU12093 Plant cDN
C 429	13	81.2	565	13	ACNA8458	ACNA8458 Cotton pr	C 501	13	81.2	912	12	ADU44593	ADU44593 Plant cDN
C 430	13	81.2	567	13	ACNS9156	ACNS9156 Cotton gy	C 502	13	81.2	915	8	ACA50774	ACA50774 Plant cDN
C 431	13	81.2	568	9	ACL20722	ACL20722 DNA clone	C 503	13	81.2	931	12	ADU42917	ADU42917 Plant cDN
C 432	13	81.2	574	9	ACL20717	ACL20717 DNA clone	C 504	13	81.2	933	6	AB199486	AB199486 Mouse jec
C 433	13	81.2	581	9	ACL20756	ACL20756 DNA clone	C 505	13	81.2	935	4	AAH69276	AAH69276 Human cer
C 434	13	81.2	582	9	ACL20762	ACL20762 DNA clone	C 506	13	81.2	937	12	ADDB0705	ADDB0705 Porcine e
C 435	13	81.2	584	9	ACL20753	ACL20753 DNA clone	C 507	13	81.2	939	5	AAH67643	AAH67643 C. glutam
C 436	13	81.2	585	9	ACL20747	ACL20747 DNA clone	C 508	13	81.2	939	8	ACA01119	ACA01119 C. glutam
C 437	13	81.2	586	9	ACL20730	ACL20730 DNA clone	C 509	13	81.2	978	13	ACNS8711	ACNS8711 Tumour-as
C 438	13	81.2	587	13	ACNS8034	ACNS8034 Cotton gy	C 510	13	81.2	978	13	ACNS8711	ACNS8711 Tumour-as
C 439	13	81.2	588	9	ACL20731	ACL20731 DNA clone	C 511	13	81.2	983	11	ACNS86135	ACNS86135 Breast ca
C 440	13	81.2	590	9	ACL20725	ACL20725 DNA clone	C 512	13	81.2	983	11	ACNS86135	ACNS86135 Breast ca
C 441	13	81.2	590	9	ACL20725	ACL20725 DNA clone	C 513	13	81.2	990	13	ADBS500	ADBS500 Aspergill
C 442	13	81.2	592	13	ACNS3574	ACNS3574 Cotton an	C 514	13	81.2	996	5	ABAI1614	ABAI1614 Human ner
C 443	13	81.2	594	6	ABK99424	ABK99424 Human CYP	C 515	13	81.2	996	6	ABK6980	ABK6980 Pancreas
C 444	13	81.2	594	6	ABK99426	ABK99426 Human CYP	C 516	13	81.2	996	6	ABK6980	ABK6980 Pancreas
C 445	13	81.2	594	6	ABK99425	ABK99425 Human CYP	C 517	13	81.2	996	6	ABK6980	ABK6980 Pancreas
C 446	13	81.2	601	6	ABK99427	ABK99427 Human CYP	C 518	13	81.2	996	13	ADBS34559	ADBS34559 DNA clone
C 447	13	81.2	605	9	ACL20700	ACL20700 DNA clone	C 519	13	81.2	1003	13	ADBS34561	ADBS34561 POSH prot
C 448	13	81.2	608	13	ACNS8014	ACNS8014 DNA clone	C 520	13	81.2	1003	13	ADBS34561	ADBS34561 POSH prot
C 449	13	81.2	608	13	ACNS8014	ACNS8014 DNA clone	C 521	13	81.2	1058	10	ADBS8512	ADBS8512 Toxicity-
C 450	13	81.2	612	9	ACL20763	ACL20763 DNA clone	C 522	13	81.2	1066	13	ADBS34560	ADBS34560 POSH prot
C 451	13	81.2	612	13	ADBS93335	ADBS93335 Novel S.	C 523	13	81.2	1083	6	AAH36765	AAH36765 DNA clone
C 452	13	81.2	613	13	ADBS7088	ADBS7088 Novel S.	C 524	13	81.2	1095	3	AAH36765	AAH36765 DNA clone
C 453	13	81.2	614	9	ACL20739	ACL20739 DNA clone	C 525	13	81.2	1110	13	ADBS47908	ADBS47908 Bacterial
C 454	13	81.2	614	9	ACL20703	ACL20703 DNA clone	C 526	13	81.2	1113	8	ABX94959	ABX94959 Rice RacB
C 455	13	81.2	621	9	ACL20751	ACL20751 DNA clone	C 527	13	81.2	1170	8	ACA26126	ACA26126 Prokaryot
C 456	13	81.2	622	2	AAK30872	AAK30872 Streptoco	C 528	13	81.2	1184	13	ADBS39447	ADBS39447 Murine S.
C 457	13	81.2	624	9	ACL20709	ACL20709 DNA clone	C 529	13	81.2	1215	9	ADA31441	ADA31441 DNA encod
C 458	13	81.2	626	9	ACL20742	ACL20742 DNA clone	C 531	13	81.2	1250	10	AAH56257	AAH56257 Murine PE

532	13	81.2	1254	8	ADA70016	Ada70016 Rice gene	C 605	13	81.2	3411	10	ADFB1485	Adfb1485 Leukemia
533	13	81.2	1317	10	ADFB58610	Adfb58610 Human pol	C 606	13	81.2	3411	12	ADQ84407	Adqg4407 Human tum
C 534	13	81.2	1342	4	AAS33102	Aas33102 DNA encod	C 607	13	81.2	3411	12	ADQ83932	Adqg3932 Human tum
C 535	13	81.2	1344	6	ABZ17335	Abz17335 Arabidops	C 608	13	81.2	3411	13	ADQ85162	Adqg5162 Human tum
536	13	81.2	1381	6	ABK84318	Abk84318 Human CDN	C 609	13	81.2	3411	13	ADQ86341	Adqg6341 Human tum
537	13	81.2	1381	10	ADD29828	Add29828 Human tum	C 610	13	81.2	3411	13	ADQ83255	Adqg3255 Human tum
538	13	81.2	1381	13	ADR25263	Adr25263 Breast ca	C 611	13	81.2	3411	13	ACN37510	Actn37510 Tumour-ab
539	13	81.2	1395	13	ADP23501	Adp23501 PRO polyP	C 612	13	81.2	3411	13	ACR99002	Actr99002 KIAA0144
540	13	81.2	1404	13	AD548622	Ad548622 Bacterial	C 613	13	81.2	3463	3	AAA40241	Aaa40241 Pig heart
541	13	81.2	1447	4	ABLO8661	Ablo8661 Drosophi1	C 614	13	81.2	3512	11	ADM01816	Adm01816 Human CDN
542	13	81.2	1471	12	AD142017	Ad142017 Plant tra	C 615	13	81.2	3525	6	ABA96529	Abag96529 G protein
543	13	81.2	1471	12	AD002568	Ad002568 Soybean o	C 616	13	81.2	3538	10	ADBS8084	Adbs8084 Toxicity-
544	13	81.2	1471	12	AD062205	Ad062205 Transcript	C 617	13	81.2	3538	10	ADBS2562	Adbs2562 Primary r
545	13	81.2	1497	4	ABL09123	Ablo9123 Drosophi1	C 618	13	81.2	3558	4	ABL09122	Ablo9122 Drosophi1
546	13	81.2	1518	13	ADT44191	Adt44191 Bacterial	C 619	13	81.2	3600	12	ADQ5194	Adq5194 Human sof
C 547	13	81.2	1525	6	ABN97321	Abn97321 Gene #381	C 620	13	81.2	3621	6	ABE67757	Abeg7757 Human int
C 548	13	81.2	1539	4	AAS33301	Aas33301 DNA encod	C 621	13	81.2	3652	12	ADO71132	Ado71132 Human BTL
C 549	13	81.2	1572	10	ADBE83553	Adbe83553 Human gen	C 622	13	81.2	3708	6	ABO79684	Abog79684 DNA seque
C 550	13	81.2	1587	6	AAD44510	Aad44510 A. variab	C 623	13	81.2	3708	10	AD050062	Ado50062 Human fat
C 551	13	81.2	1599	11	AD132079	Ad132079 Human CDN	C 624	13	81.2	3741	11	AD077948	Ado77948 Brascica
C 552	13	81.2	1613	4	AAH17591	Aah17591 Human CDN	C 625	13	81.2	3795	4	AAK91702	Aak91702 Mouse fat
553	13	81.2	1629	11	AD131202	Ad131202 Human CDN	C 626	13	81.2	3798	10	ABX08985	Abx08985 CDNA enc
554	13	81.2	1677	10	AD108124	Adc08124 Rice DNA	C 627	13	81.2	3809	4	ABL08660	Ablo8660 Drosophi1
555	13	81.2	1686	10	ADFO0666	Adfo0666 Bacterial	C 628	13	81.2	3813	4	AAH62794	Aah62794 Strimp wh
556	13	81.2	1726	12	ADQ22650	Adq22650 Human sof	C 629	13	81.2	3832	8	ABX95221	Abx95221 CDNA enc
557	13	81.2	1741	6	ABK34581	Abk34581 Human CDN	C 630	13	81.2	4014	6	ABSS56829	Abss56829 Human mac
558	13	81.2	1759	13	ADRO7047	Adro7047 Full leng	C 631	13	81.2	4037	10	ADBS4117	Adbs4117 Human pro
C 559	13	81.2	1776	5	ADL63723	Adl63723 Human ova	C 632	13	81.2	4037	8	ABX34529	Abx34529 Human mdd
C 560	13	81.2	1823	12	ADH13780	Adh13780 Human ENZ	C 633	13	81.2	4130	12	AD877047	Ad877047 Human CDN
C 561	13	81.2	1849	6	ABL60567	Ablo60567 Human str	C 634	13	81.2	4132	12	ADU60217	Adu60217 Conceteme
C 562	13	81.2	1887	10	ADFE60139	Adfe60139 Human con	C 635	13	81.2	4132	12	AD045706	Ado45706 Human o11
C 563	13	81.2	1962	8	ACAS2961	Acas2961 Prokaryot	C 636	13	81.2	4240	12	AD064490	Adog64490 Novel hum
C 564	13	81.2	1979	5	ABA15720	Abal5720 Human ner	C 637	13	81.2	4361	6	AA934758	Aa934758 Human DNA
C 565	13	81.2	2052	12	ADO80792	Ado80792 Porcine e	C 638	13	81.2	4381	6	ABK82001	Abk82001 CDNA enc
C 566	13	81.2	2119	4	AA1818159	AA1818159 Human pol	C 639	13	81.2	4403	2	AAQ47927	Aaq47927 Ratred ba
C 567	13	81.2	2119	5	ADQ98365	Adq98365 DNA encod	C 640	13	81.2	4403	6	ABN95905	Abn95905 Gene #240
C 568	13	81.2	2119	9	ADBA48125	Adba48125 Novel hum	C 641	13	81.2	4403	10	ADDL14775	Addl14775 Human strc
569	13	81.2	2151	12	ADH404227	Adh404227 DNA encod	C 642	13	81.2	4403	13	ADNR4926	Adnr4926 Breast ca
570	13	81.2	2163	12	ADH45317	Adh45317 Human enz	C 643	13	81.2	4553	11	ADN95173	Adn95173 Human BEC
571	13	81.2	2212	6	ABK35505	Abk35505 Human end	C 644	13	81.2	4632	4	ABL24793	Ablo24793 Drosophi1
C 572	13	81.2	2286	6	AAAL54057	AA154057 CDNA enc	C 645	13	81.2	4743	4	ABL27036	Ablo27036 Drosophi1
573	13	81.2	2311	13	ACN40495	Actn40495 Tumour-ab	C 646	13	81.2	4767	2	AAZ10358	Aaz10358 Partia1 g
574	13	81.2	2372	10	ADBE2473	Adbe2473 Human CDN	C 647	13	81.2	5071	4	AAK74516	Aak74516 Human imm
575	13	81.2	2440	8	ABX49950	Abx49950 Human CDN	C 648	13	81.2	5071	6	ABK69831	Abk69831 Human sec
C 576	13	81.2	2460	12	ADP29128	Adp29128 Human sec	C 649	13	81.2	5072	6	AAK74517	Aak74517 Human imm
C 577	13	81.2	2469	10	ADBE1853	Adbe1853 Human CDN	C 650	13	81.2	5072	6	ABK69833	Abk69833 Human sec
C 578	13	81.2	2601	8	ACA32877	Acta32877 Prokaryot	C 651	13	81.2	5109	4	ABLI77409	Abli77409 Drosophi1
C 579	13	81.2	2604	4	AAS52920	Aas52920 Enterococ	C 652	13	81.2	5176	6	ABA91397	Abag91397 Arabidops
C 580	13	81.2	2713	8	ACA57245	Acta57245 Human adi	C 653	13	81.2	5537	4	AAK84869	Aak84869 Human imm
581	13	81.2	2716	13	ADRO7710	Adro7710 Full leng	C 654	13	81.2	5608	6	ABL64381	Ablo64381 Stomach c
C 582	13	81.2	2730	10	ADA52805	Ada52805 Human cod	C 655	13	81.2	5608	6	ABN95262	Abn95262 Gene #176
C 583	13	81.2	2835	8	ABZ77166	Abz77166 Phoma dec	C 656	13	81.2	6835	2	AAK13141	Aak13141 Enterococ
584	13	81.2	2839	12	ADQ63879	Adq63879 Novel hum	C 657	13	81.2	6835	6	AB938936	Ab938936 Enterococ
585	13	81.2	2868	8	AAT85578	Aat85578 Murine WS	C 658	13	81.2	6941	13	ADP24242	Adp24242 PEO polyP
586	13	81.2	2868	8	ACA75468	Acta75468 Mouse DNA	C 659	13	81.2	6949	13	ADR84336	Adr84336 Aspergill
587	13	81.2	2868	9	ACH66774	Ach66774 Mouse par	C 660	13	81.2	6994	10	ADFR1696	Adfr1696 Leukemia
588	13	81.2	2868	10	ADCO8909	Adco8909 Partia1 m	C 661	13	81.2	7210	12	ADL67020	Adl67020 Novel lac
589	13	81.2	2923	8	ABT42538	Abt42538 Human nuc	C 662	13	81.2	7232	4	ABL24792	Ablo24792 Drosophi1
C 590	13	81.2	2931	12	ADQ67246	Adq67246 Novel hum	C 663	13	81.2	8200	10	ADFS4889	Adfs4889 Human CYP
C 591	13	81.2	2952	12	ADP29129	Adp29129 Human sec	C 664	13	81.2	8200	10	ADFR1696	Adfr1696 Toxicity
C 592	13	81.2	3114	13	ADR25347	Adr25347 Breast ca	C 665	13	81.2	8921	10	ABT42465	Abt42465 Toxicity
C 593	13	81.2	3132	6	AA94759	Aa94759 Human DNA	C 666	13	81.2	8957	4	AAK69134	Aak69134 Human imm
C 594	13	81.2	3132	12	ADQ21319	Adq21319 Human sof	C 667	13	81.2	8957	4	AAK69134	Aak69134 Human imm
C 595	13	81.2	3140	4	ABL27038	Ablo27038 Drosophi1	C 668	13	81.2	9180	6	AAV57416	Aav57416 Tumour su
C 596	13	81.2	3143	13	ADK41001	Adk41001 Novel hum	C 669	13	81.2	9180	6	ABN96954	Abn96954 Gene #346
C 597	13	81.2	3143	10	ADR15715	Adr15715 Klnase 36	C 670	13	81.2	9180	12	ADQ21304	Adq21304 Human sof
598	13	81.2	3206	8	ABX71060	Abx71060 Novel hum	C 671	13	81.2	10862	2	AAV34396	Aav34396 Drosophi1
599	13	81.2	3259	13	ACN39223	Actn39223 Tumour-ab	C 672	13	81.2	10862	6	ABA04030	Abao4030 Flaviviru
C 600	13	81.2	3265	4	ABLO4138	Ablo4138 Drosophi1	C 673	13	81.2	10862	12	ADJ57393	Adj57393 Hamster p
601	13	81.2	3273	10	ADBA7326	Adba7326 Human CDN	C 674	13	81.2	10882	4	AAK83821	Aak83821 Chimeric
602	13	81.2	3274	8	ABK62936	Abk62936 Human act	C 675	13	81.2	10882	4	AAK83821	Aak83821 Chimeric
C 603	13	81.2	3411	6	ABK83684	Abk83684 Human CDN	C 676	13	81.2	11839	4	AALO9490	Aalo9490 Human rep
C 604	13	81.2	3411	6	ABN95213	Abn95213 Gene #171	C 677	13	81.2	11839	4	ABL97834	Ablo97834 Human tes

[illegible]

824	12	75.0	32	6	AAD25631	Ad25631 Oligo #11	C 897	12	75.0	386	4	AAK01591	Aak01591 Human bra
825	12	75.0	32	6	AAD25629	Ad25629 Oligo #9	C 898	12	75.0	386	4	ABS26620	Ab26620 Human liv
826	12	75.0	32	6	AAD25627	Ad25627 Oligo #7	C 899	12	75.0	386	5	AAI01561	Aai01561 Human #15
827	12	75.0	41	2	AAV65931	Av65931 Oligonuclei	C 900	12	75.0	387	5	AAV65293	Av65293 Novel hum
828	12	75.0	41	7	ADI93044	Adi93044 Hepatitis	C 901	12	75.0	387	5	AAI13376	Aai13376 Probe #33
829	12	75.0	43	6	ADBS3001	Adbs3001 FEN-1 rel	C 902	12	75.0	382	4	ABAS5073	Abas5073 Human foe
C 830	12	75.0	53	12	ADN36217	Adn36217 Probe #29	C 903	12	75.0	382	4	AAI34730	Aai34730 Probe #34
C 831	12	75.0	53	12	ADN36055	Adn36055 Probe #13	C 904	12	75.0	392	4	ABAA4622	Abaa4622 Human.bre
C 832	12	75.0	64	2	AAK34322	Aak34322 Human bet	C 905	12	75.0	392	4	ABA24826	Ab24826 Probe #32
C 833	12	75.0	65	6	ABN33049	Abn33049 Rat splic	C 906	12	75.0	392	4	AAK28789	Aak28789 Human bon
C 834	12	75.0	65	6	ABN30919	Abn30919 Rat splic	C 907	12	75.0	382	4	AAK03338	Aak03338 Human bra
C 835	12	75.0	100	8	ACD78395	Ac78395 E. coli K	C 908	12	75.0	382	4	ABBS28393	Abbs28393 Human liv
C 836	12	75.0	126	3	AAAI8203	Aaci8203 Human sec	C 909	12	75.0	382	5	AAI03270	Aai03270 Probe #32
C 837	12	75.0	141	6	ABN60348	Abn60348 Human can	C 910	12	75.0	392	6	ABSO3316	Abso3316 Human gen
C 838	12	75.0	144	10	ADF73102	Adf73102 Nucleotid	C 911	12	75.0	392	6	ACL13223	Ac113223 DNA clone
C 839	12	75.0	149	12	AD013517	Ad013517 SNP targe	C 912	12	75.0	395	12	AD016406	Ad016406
C 840	12	75.0	158	9	ACL13377	Ac113377 DNA clone	C 913	12	75.0	386	4	AAV94868	Av94868 Human ova
C 841	12	75.0	177	2	AAQ72531	Aaq72531 Osteoclas	C 914	12	75.0	386	6	ABL48818	Ab148818 Ovarian c
C 842	12	75.0	177	6	ABN86720	Abn86720 Human ovt	C 915	12	75.0	386	6	ABT03135	Abt03135 Human ova
C 843	12	75.0	185	6	AAD37113	Ad37113 Human pho	C 916	12	75.0	386	11	ADM10728	Adm10728 Human ova
C 844	12	75.0	189	7	ADS69752	Ad69752 Corn seed	C 917	12	75.0	386	12	ADJ11058	Adj11058 Represent
C 845	12	75.0	219	4	AAI27063	Aai27063 Probe #16	C 918	12	75.0	386	12	ADM43319	Adm43319 Human ova
C 846	12	75.0	219	4	ABA75333	Ab75333 Human foe	C 919	12	75.0	387	8	ABX37270	Abx37270 Bovine ES
C 847	12	75.0	219	4	AAI55899	Aai55899 Probe #24	C 920	12	75.0	388	4	AAI23887	Aai23887 Probe #13
C 848	12	75.0	219	4	ABA33978	Ab33978 Probe #18	C 921	12	75.0	388	4	AAI14693	Aai14693 Probe #46
C 849	12	75.0	219	4	AAK49962	Aak49962 Human bon	C 922	12	75.0	398	4	ABAA69006	Abaa69006 Human foe
C 850	12	75.0	219	4	AAK23888	Aak23888 Human bra	C 923	12	75.0	398	4	ABAA66425	Abaa66425 Human foe
C 851	12	75.0	219	4	ABSA49609	Ab49609 Human liv	C 924	12	75.0	388	4	AAI49195	Aai49195 Probe #17
C 852	12	75.0	219	6	ABSS2452	Ab2452 Human gen	C 925	12	75.0	388	4	AAI36060	Aai36060 Probe #47
C 853	12	75.0	223	8	ABX52786	Abx52786 Bovine ES	C 926	12	75.0	388	4	ABAA45898	Abaa45898 Human bra
C 854	12	75.0	226	2	AAK39488	Aak39488 Human sec	C 927	12	75.0	388	4	ABAA51016	Abaa51016 Human bra
C 855	12	75.0	240	6	ABL83299	Ab183299 Human ova	C 928	12	75.0	388	4	ABAA51950	Abaa51950 Probe #14
C 856	12	75.0	242	6	ABN17691	Abn17691 Human ORF	C 929	12	75.0	388	4	ABAA26057	Abaa26057 Probe #45
C 857	12	75.0	243	12	ADL03735	Adl03735 DNA. enco	C 930	12	75.0	388	4	AAK30097	Aak30097 Human bon
C 858	12	75.0	253	6	ABL78183	Ab178183 Human ova	C 931	12	75.0	388	4	AAK43118	Aak43118 Human bon
C 859	12	75.0	257	6	ABL87535	Ab187535 Human ova	C 932	12	75.0	388	4	AAK04590	Aak04590 Human bra
C 860	12	75.0	257	6	ABL84726	Ab184726 Human ova	C 933	12	75.0	388	4	AAK17325	Aak17325 Human bra
C 861	12	75.0	258	11	ADL98233	Adl98233 Human tum	C 934	12	75.0	388	4	ABSA42752	Ab42752 Human liv
C 862	12	75.0	279	9	ACL13313	Ac113313 DNA clone	C 935	12	75.0	388	4	ABSA29747	Ab29747 Human liv
C 863	12	75.0	284	6	ABL72537	Ab172537 Corn tass	C 936	12	75.0	388	5	AAI04499	Aai04499 Probe #44
C 864	12	75.0	287	10	ABX84480	Abx84480 Corn ear-	C 937	12	75.0	388	5	AAI09489	Aai09489 Probe #94
C 865	12	75.0	290	6	ABL73350	Ab173350 Corn tass	C 938	12	75.0	388	6	ABSI17192	Ab17192 Human gen
C 866	12	75.0	290	6	ACL13357	Ac113357 DNA clone	C 939	12	75.0	388	6	ABSO4676	Abso4676 Human gen
C 867	12	75.0	308	6	ABL87220	Ab187220 Human ova	C 940	12	75.0	388	6	AAI91430	Aai91430 Human pol
C 868	12	75.0	310	4	AAK89338	Aak89338 Human imm	C 941	12	75.0	404	8	ABZ56406	Abz56406 Aspergill
C 869	12	75.0	313	6	ABO98681	Ab98681 Human ORF	C 942	12	75.0	404	9	ACL13341	Ac113341 DNA clone
C 870	12	75.0	319	10	ADF85706	Adf85706 Human ade	C 943	12	75.0	405	13	ACN61537	Acn61537 Cotton gy
C 871	12	75.0	320	6	ABL66069	Ab166069 Lung canc	C 944	12	75.0	407	2	AAZ34254	Aaz34254 Human EST
C 872	12	75.0	322	9	ACL13369	Ac113369 DNA clone	C 945	12	75.0	407	3	AACT78564	Aact78564 Human EST
C 873	12	75.0	323	4	AAI98608	Aai98608 Human exc	C 946	12	75.0	407	8	ACA63822	Aca63822 Novel hum
C 874	12	75.0	323	5	AAI63004	Aai63004 Human kid	C 947	12	75.0	407	8	ACA71986	Aca71986 Human PRO
C 875	12	75.0	326	9	ACL13335	Ac113335 DNA clone	C 948	12	75.0	407	8	ABX92626	Abx92626 Human PRO
C 876	12	75.0	328	6	ABV94088	Abv94088 Breast ca	C 949	12	75.0	407	8	ACA63637	Aca63637 Human sec
C 877	12	75.0	332	9	ACL13316	Ac113316 DNA clone	C 950	12	75.0	407	9	ADA24970	Ada24970 Novel hum
C 878	12	75.0	334	3	AAAC13254	AAc13254 DNA clone	C 951	12	75.0	407	9	ACD29968	Ac29968 Novel hum
C 879	12	75.0	344	3	AAAC06746	AAc06746 Human sec	C 952	12	75.0	407	9	ADA12631	Ada12631 Human sec
C 880	12	75.0	346	5	ABAI3740	Abai3740 Human ner	C 953	12	75.0	407	9	ACD29383	Ac29383 Novel hum
C 881	12	75.0	351	4	ABA06677	Ab06677 Human CDN	C 954	12	75.0	407	9	ACL13331	Ac113331 DNA clone
C 882	12	75.0	351	6	ABV84014	Abv84014 Human pol	C 955	12	75.0	407	10	ADB73937	Adb73937 Human PRO
C 883	12	75.0	354	2	AAV04511	Aav04511 Osteoclas	C 956	12	75.0	407	10	ADB76653	Adb76653 Human PRO
C 884	12	75.0	361	9	ACL13372	Ac113372 DNA clone	C 957	12	75.0	407	10	ADC44079	Adc44079 Human EST
C 885	12	75.0	364	10	ADD27665	Ad27665 Human adt	C 958	12	75.0	407	10	ADC61839	Adc61839 Human EST
C 886	12	75.0	367	9	ACL13330	Ac113330 DNA clone	C 959	12	75.0	407	10	ADC63803	Adc63803 Human EST
C 887	12	75.0	372	2	ACL13270	Ac113270 DNA clone	C 960	12	75.0	407	10	ADC66903	Adc66903 Human EST
C 888	12	75.0	376	2	AAK33548	Aak33548 Human sec	C 961	12	75.0	407	10	ADC69027	Adc69027 Human EST
C 889	12	75.0	376	10	ADK56201	Adk56201 Plant DNA	C 962	12	75.0	407	10	ADC63087	Adc63087 Human EST
C 890	12	75.0	378	5	ABV18153	Abv18153 Human pro	C 963	12	75.0	407	10	ADC68152	Adc68152 Human EST
C 891	12	75.0	385	6	ABK45359	Abk45359 CDNA enco	C 964	12	75.0	407	10	ADC41472	Adc41472 Human EST
C 892	12	75.0	386	4	AAI11634	Aai11634 Probe #15	C 965	12	75.0	407	10	ADC67527	Adc67527 Human EST
C 893	12	75.0	386	4	ABAA53326	Abaa53326 Human foe	C 966	12	75.0	407	10	ADC62463	Adc62463 Human EST
C 894	12	75.0	386	4	ABAA2905	Abaa2905 Human bre	C 967	12	75.0	407	10	ADC42096	Adc42096 Human EST
C 895	12	75.0	386	4	ABA23103	Ab23103 Probe #15	C 968	12	75.0	407	10	ADBA49465	Adba49465 Human EST
C 896	12	75.0	386	4	AAK27034	Aak27034 Human bon	C 969	12	75.0	407	10	ADBS5519	Adbs5519 Human EST

C 970	12	75.0	407	10	AD616633	AD616633 Human EST
C 971	12	75.0	407	10	ADD73248	ADD73248 Human EST
C 972	12	75.0	407	10	ADD72606	ADD72606 Human EST
C 973	12	75.0	407	10	AD617257	AD617257 Human EST
C 974	12	75.0	407	10	AD647271	AD647271 Human EST
C 975	12	75.0	407	10	ADG53028	ADG53028 Human EST
C 976	12	75.0	407	10	ADG60348	ADG60348 Human EST
C 977	12	75.0	407	10	AD616108	AD616108 Human EST
C 978	12	75.0	407	10	ACD42787	ACD42787 Novel hum
C 979	12	75.0	407	12	AD648765	AD648765 Human EST
C 980	12	75.0	407	12	AD689866	AD689866 Human EST
C 981	12	75.0	407	12	AD661506	AD661506 Human EST
C 982	12	75.0	407	12	AD640198	AD640198 Human EST
C 983	12	75.0	407	12	AD645994	AD645994 Human EST
C 984	12	75.0	407	12	AD624390	AD624390 Human EST
C 985	12	75.0	407	12	AD640822	AD640822 Human EST
C 986	12	75.0	407	12	AD623766	AD623766 Human EST
C 987	12	75.0	407	12	AD623749	AD623749 Human EST
C 988	12	75.0	407	12	AD627216	AD627216 Human EST
C 989	12	75.0	407	12	AD627852	AD627852 Human EST
C 990	12	75.0	407	12	AD641446	AD641446 Human EST
C 991	12	75.0	407	12	AD6F3125	AD6F3125 Human EST
C 992	12	75.0	407	12	AD6F2491	AD6F2491 Human EST
C 993	12	75.0	407	12	AD6F2592	AD6F2592 Human EST
C 994	12	75.0	407	12	AD6F34381	AD6F34381 Human EST
C 995	12	75.0	407	12	AD6F4618	AD6F4618 Human EST
C 996	12	75.0	407	12	ADG50604	ADG50604 Human EST
C 997	12	75.0	407	12	ADG49980	ADG49980 Human EST
C 998	12	75.0	407	12	ADG51852	ADG51852 Human EST
C 999	12	75.0	407	12	ADG49356	ADG49356 Human EST
C1000	12	75.0	407	12	ADG48732	ADG48732 Human EST

ALIGNMENTS

RESULT 1
AAT18256
ID AAT18256 standard; DNA, 16 BP.

XX	AC	AAT18256;
XX	DT	17-SEP-1996 (first entry)
XX	DE	HBV epsilon encapsidation mRNA intermediate antisense oligo L2c.
XX	KW	Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
KW	epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;	
KW	treatment; chronic infection; modulation; translation; transcription;	
KW	release; host cell; ss.	
XX	OS	Synthetic.
XX	PN	W09603152-A1.
XX	PD	08-FEB-1996.
XX	PF	28-JUL-1995; 95WO-US009143.
XX	PR	28-JUL-1994; 94US-00281106.
XX	PA	(GEOU) UNIV GEORGETOWN.
XX	PI	Korba BR, Gerin JL;
XX	XX	WPI, 1996-116796/12.

Single stranded oligo:nucleotide(s) for inhibiting replication of hepatitis B virus - are anti-sense to portions of the epsilon encapsidation sequence and modulate HBV function.

Claim 15; Page 44; 56pp; English.

The present sequence, which inhibits the replication of hepatitis B virus (HBV) in a host cell, is a single stranded antisense oligonucleotide that binds the epsilon encapsidation sequence of a mRNA intermediate derived from the HBV genome. The 1st nucleotide of the oligonucleotide corresponds to nucleotide 1894 of the HBV ayw subtype C gene, using the numbering scheme from the sequence published by Galibert et al., Nature 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to treat chronic HBV infection by modulating a HBV related function, e.g. translation, transcription, encapsidation, replication and release from a host cell. The effect of the oligonucleotide on the levels of HBV DNA in the extracellular medium (VIR. DNA), intracellular viral replicative intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core CC treatment) or ND (not determined), given as the EC(90) (microm, 9 days of RNA (>20), HBsAg (>20), HBeAg (>20) and HBeAg (18.5).

Query Match 100.0%; Score 16; DB 2; Length 16;
Best local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGCA 16
Db 1 AAAGCCACCCCAAGCA 16

RESULT 2
AAV14125
ID AAV14125 standard; DNA, 16 BP.

XX	AC	AAV14125;
XX	DT	27-APR-2003 (revised)
XX	DT	19-MAY-1998 (first entry)
XX	DE	Probe HBPr41 for preCore region of HBV.

Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target;

KW mutation detection; ss.

XX	OS	Synthetic.
XX	OS	Hepatitis B virus.
XX	PN	W09740193-A2.
XX	PD	30-OCT-1997.
XX	PF	21-APR-1997; 97WO-EP002002.
XX	PR	19-APR-1996; 96EP-00870053.
XX	PA	(INNO-) INNOGENETICS NV.
XX	PI	Stuyver L, Rossau R, Maertens G;
XX	XX	WPI, 1997-535867/49.

Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.

Claim 5; Page 27; 80pp; English.

This sequence represents a probe for the preCore region of hepatitis B virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleotide acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridizing (I) with a combination of at least

CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected for treatment with drugs, e.g. lamivudine and
 CC penciclovir. (updated on 27-AUG-2003 to correct OS field.)

XX Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
 1 AAAGCCACCCAGGCA 16

Db 1 AAAGCCACCCAGGCA 16

RESULT 3

ID ADB68575 standard; DNA; 16 BP.

XX ADB68575;

AC 04-DEC-2003 (first entry)

DT NG3 A-L-P conjugate DNA component used to target HBV e-site.

XX homogeneous A-L-P conjugate; hepatic; chronic viral hepatitis; cirrhosis;
 KM malaria; viral infection; protozoan; cancer; hepatocellular carcinoma;
 KM HCC; ss; NG3; HBV; e-site; pregenome.

XX Hepatitis B virus.

FT Key location/Qualifiers

FT modified_base 1..16

FT /*tag= b /mod_base= OTHER

FT /note= "OTHER = phosphorothioate backbone"

FT modified_base 1

FT /*tag= a /mod_base= OTHER

FT /note= "OTHER = Optionally linked to YEE(a)G(a)N(a)C)3-SMCC

FT and various chemical groups as shown in figures"

FT modified_base 16

FT /*tag= c /mod_base= OTHER

FT /note= "OTHER = Optionally linked to chemical group as

FT shown in figure 5"

XX WO2003067209-A2.

XX 14-AUG-2003.

XX 21-JUN-2002; 2002WO-US019908.

XX 22-JUN-2001; 2001US-00888164.

XX (CELL-) CELL WORKS INC.

XX (UYJO) UNITV JOHNS HOPKINS.

XX Te'o POP, Duff R, Zhou Y, Deamond S, Roby C;

XX WPI; 2003-697456/66.

XX New homogeneous prodrgng conjugate containing hepatic ligand for delivery

XX of pathogen-specific oligomer useful for treating liver infections or

XX cancer.

XX Claim 7; Page 83; 107bp; English.

XX The invention relates to a novel homogeneous conjugate comprising a

XX hepatic ligand, bifunctional linker and biologically stable oligomer that

XX binds to a sequence in a hepatic virus or pathogen and is released from

XX the conjugate by hydrolysis or reduction. The conjugate of the invention

XX may be useful during the treatment of liver diseases including chronic

XX viral hepatitis, cirrhosis, malaria, viral or protozoan infection and

XX cancer, such as hepatocellular carcinoma (HCC). The current sequence is

XX that of the NG3 A-L-P conjugate DNA component of the invention which was

XX used to target the Hepatitis B virus (HBV) pregenome (e-site).

XX Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
 1 AAAGCCACCCAGGCA 16

Db 1 AAAGCCACCCAGGCA 16

RESULT 4

ID ACD55710/c standard; RNA; 17 BP.

XX ACD55710;

AC 23-SEP-2003 (first entry)

DT HBV amberyzyme substrate sequence #183.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KM RNA stability; RNA expression; RNA synthesis; antisense;
 KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;

KM amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;

KM HBV reverse transcriptase; Enhancer I region; viral replication;

KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;

KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KM virucide; antiinflammatory; substrate; ss.

XX Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT) BLATT L.

XX (MACE/) MACEJAK D.

XX (MCSW/) MCSWIGEN J.

XX (MORR/) MORRISSEY D.

XX (PAVC/) PAVCO P.

XX (LEEP/) LEE P.

XX (DRAP/) DRAPER K.

XX (ROBE/) ROBERTS E.

XX Blact L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;

XX Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

2PA (RIBO-) RIBOZYME PHARM INC
2PA (BLAT/) BLATT L.
2PA (MACE/) MACEJAK D.
2PA (MCSW/) MCSWIGGEN J.
2PA (MORR/) MORRISSEY D.

PR	14-MAY-1992;	92US-00882712
PR	07-FEB-1994;	94US-00193627
PR	08-NOV-1999;	99US-00436430
PR	20-MAR-2000;	2000US-00531025

```
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (MORR/) MORRISSEY D.
XX
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
XX PT specifically cleaving RNA derived from hepatitis B virus and comprising
XX PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX PS Disclosure; SEQ ID NO 1755; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
XX CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
XX CC comprising one or more binding arms, without requiring the presence of a
XX CC 2'-OH group within the molecule for activity. The nucleic acids are
XX CC useful for treating hepatitis B virus infection, hepatitis,
XX CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
XX CC combination with other therapies such as lamivudine and interferons. The
XX CC nucleic acids are useful as diagnostic tools to examine genetic drift and
XX CC mutations within diseased cells, for detecting the presence of HBV RNA in
XX CC a cell, for the study of RNA and for down-regulating gene expression of
XX CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
XX CC sequence represents an HBV RNA target sequence, used in the scope of the
XX CC invention. Note: The sequence data for this patent is also available in
XX CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 12; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAAGCCACCCAGGCA 16
XX 16 AAAGCCACCCAGGCA 1
XX
XX Db
XX
XX RESULT 7
XX ADM60244/c
XX ID ADM60244 standard; RNA; 17 BP.
XX
XX AC ADM60244;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Hepatitis B virus (HBV) RNA target sequence #2378.
XX
XX KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
XX KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
XX KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
XX KW virulence; hepatotropic; antiinflammatory; cytosstatic.
XX
XX OS Hepatitis B virus.
XX
XX PN US2004054156-A1.
XX
XX PD 18-MAR-2004.
XX
XX PF 15-JAN-2003; 2003US-00342902.
XX
XX PR 14-MAY-1992; 92US-00882712.
XX PR 07-FEB-1994; 94US-00193627.
XX PR 08-NOV-1999; 99US-00436430.
XX PR 20-MAR-2000; 2000US-00531025.
XX PR 09-AUG-2000; 2000US-00636385.
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```
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (MORR/) MORRISSEY D.
XX
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
XX PT specifically cleaving RNA derived from hepatitis B virus and comprising
XX PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX PS Disclosure; SEQ ID NO 2378; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
XX CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
XX CC comprising one or more binding arms, without requiring the presence of a
XX CC 2'-OH group within the molecule for activity. The nucleic acids are
XX CC useful for treating hepatitis B virus infection, hepatitis,
XX CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
XX CC combination with other therapies such as lamivudine and interferons. The
XX CC nucleic acids are useful as diagnostic tools to examine genetic drift and
XX CC mutations within diseased cells, for detecting the presence of HBV RNA in
XX CC a cell, for the study of RNA and for down-regulating gene expression of
XX CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
XX CC sequence represents an HBV RNA target sequence, used in the scope of the
XX CC invention. Note: The sequence data for this patent is also available in
XX CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 12; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAAGCCACCCAGGCA 16
XX 17 AAAGCCACCCAGGCA 2
XX
XX Db
XX
XX RESULT 8
XX AAT71786
XX ID AAT71786 standard; DNA; 18 BP.
XX
XX AC AAT71786;
XX
XX DT 29-AUG-1997 (first entry)
XX
XX DE Hepatitis B virus precore antigen wild-type target sequence primer.
XX
XX KW HBV; ligase chain reaction; internal standard; amplification; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_difference 1
XX FT /*tag= a
XX FT /note= "Phosphorylated"
XX FT misc_difference 18
XX FT /*tag= b
XX FT /note= "Haptenated with fluorescein"
XX
XX MO9640996-A1.
XX
XX PD 19-DEC-1996.
XX
XX PF 03-JUN-1996; 96WO-US008429.
XX PR 07-JUN-1995; 95US-00480220.
```

XX (ABBO) ABBOTT LAB.
 XX Birkenmeyer L, Mushahwar IK;
 XX WPI, 1997-052367/05.
 DR Quantitative detection of target nucleic acid sequence, esp. hepatitis B
 XX virus - can distinguish wild-type and mutant DNA types.
 XX
 PS Claim 14; Page 29; 40pp; English.
 CC A novel method has been produced for detecting the amount of a target
 CC nucleic acid sequence which may be present in a test sample. It involves
 CC contacting the test sample with means for performing a nucleic acid
 CC amplification reaction; and determining the ratio of target amplification
 CC products to internal standard amplification products present in the
 CC sample. The present sequence represents a primer/target specific probe
 CC for the hepatitis B virus (HBV) precore antigen wild-type target sequence
 CC (AAV71783). The method can be used for distinguishing between two
 CC different nucleic acid sequences present in a sample e.g. wild-type and
 CC mutant. The compositions can be used for quantitatively detecting the DNA
 CC of HBV
 CC
 SQ Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16
 RESULT 9
 ID AAV14133 standard; DNA; 18 BP.
 AC AAV14133;
 XX
 DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 DE Probe HBPr49 for precore region of HBV.
 XX
 KW Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis;
 KW precore region; HBsAg region; genotype specific target;
 XX mutation detection; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO9740193-A2.
 XX
 PD 30-OCT-1997.
 XX
 PF 21-APR-1997; 97WO-EP002002.
 XX
 PR 19-APR-1996; 96EP-00870053.
 XX
 PA (INNO-) INNOGENETICS NV.
 PA
 PI Stuyver L, Rossau R, Maertens G;
 PI WPI, 1997-535867/49.
 DR
 XX
 XX
 PT Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, precore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 PS Claim 5; Page 27; 80pp; English.
 XX

CC This sequence represents a probe for the precore region of hepatitis B
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (I) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (I) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV precore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, precore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 CC
 SQ Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16
 RESULT 10
 ID AAT71785/c
 XX AAT71785 standard; DNA; 19 BP.
 AC AAT71785;
 XX
 DT 29-AUG-1997 (first entry)
 XX
 DE Hepatitis B virus precore antigen wild-type target sequence primer.
 XX
 KW HBV; ligase chain reaction; internal standard; amplification; ss.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT misc_difference 1 /*tag= a
 FT /note= "Haptenated with fluorescein"
 XX
 PN WO9640996-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US008429.
 XX
 PR 07-JUN-1995; 95US-00480220.
 XX
 PA (ABBO) ABBOTT LAB.
 PA
 PI Birkenmeyer L, Mushahwar IK;
 PI WPI, 1997-052367/05.
 DR
 XX
 XX
 PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
 PT virus - can distinguish wild-type and mutant DNA types.
 XX
 PS Claim 14; Page 29; 40pp; English.
 XX
 CC A novel method has been produced for detecting the amount of a target
 CC nucleic acid sequence which may be present in a test sample. It involves
 CC contacting the test sample with means for performing a nucleic acid
 CC amplification reaction; and determining the ratio of target amplification
 CC products to internal standard amplification products present in the

CC sample. The present sequence represents a primer/target specific probe
CC for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC (AAAT1783). The method can be used for distinguishing between two
CC different nucleic acid sequences present in a sample e.g. wild-type and
CC mutant. The compositions can be used for quantitatively detecting the DNA
CC of HBV

XX Sequence 19 BP; 0 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGCA 16
18 AAAGCCACCCAGCA 3

RESULT 11

AAAT1789/c

ID AAAT1789 standard; DNA; 19 BP.

AC AAAT1789;

DT 29-AUG-1997 (first entry)

XX Hepatitis B virus precore antigen mutant target sequence primer.

XX HBV, ligase chain reaction; internal standard; amplification; ss.

XX Synthetic.

FT Key Location/Qualifiers

FT misc_difference 1/*tag= a
/note= "Haptenated with fluorescein"

PN MO9640996-A1.

PD 19-DEC-1996.

XX 03-JUN-1996; 96MO-US008429.

PR 07-JUN-1995; 95US-00480220.

XX (ABBO) ABBOTT LAB.

PI Birkenmeyer L, Mushahwar IK;

DR WPI; 1997-052367/05.

PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT virus - can distinguish wild-type and mutant DNA types.

XX Claim 14; Page 30; 40pp; English.

CC A novel method has been produced for detecting the amount of a target
CC nucleic acid sequence which may be present in a test sample. It involves
CC contacting the test sample with means for performing a nucleic acid
CC amplification reaction, and determining the ratio of target amplification
CC products to internal standard amplification products present in the
CC sample. The present sequence represents a primer/target specific probe
CC for the hepatitis B virus (HBV) precore antigen mutant target sequence
CC (AAAT1784). The method can be used for distinguishing between two
CC different nucleic acid sequences present in a sample e.g. wild-type and
CC mutant. The compositions can be used for quantitatively detecting the DNA
CC of HBV

XX Sequence 19 BP; 1 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGCA 16
18 AAAGCCACCCAGCA 3

RESULT 12

ADM00160/c

ID ADM00160 standard; RNA; 19 BP.

AC ADM00160;

DT 20-MAY-2004 (first entry)

XX Hepatitis B virus short interfering nucleic acid (siNA) #576.

XX siNA; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;

XX Hepatitis B virus.

XX US2003206687-A1.

XX 06-NOV-2003.

XX 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.

XX 07-FEB-1994; 94US-00193627.

XX 08-NOV-1999; 99US-00436430.

XX 20-MAR-2000; 2000US-00531025.

XX 09-AUG-2000; 2000US-00636385.

XX 24-OCT-2000; 2000US-00696347.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002MO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX (MORR/) MORRISSEY D.

XX (MCSW/) MCSWIGEN J A.

XX (BEIG/) BEIGELMAN L.

XX Morrissey D, Mcswigen JA, Beigelman L;

DR WPI; 2003-901032/82.

PT New short interfering nucleic acid molecules which down-regulates
PT expression of a hepatitis B virus (HBV) or which inhibits HBV
PT replication, useful for treating human HBV infections or for
PT characterizing gene function.

XX Claim 11; Page 48; 72pp; English.

CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv) a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA

CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprises separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

SO Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;
 Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCAAGCA 16
 DB 16 AAAGCCACCAAGCA 1

RESULT 13
 ADM00806
 ID ADM00806 standard; RNA; 19 BP.

AC ADM00806;
 DT 20-MAY-2004 (first entry)
 XX
 DE Hepatitis B virus short interfering nucleic acid (siNA) #1222.

XX
 KM Vincide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.

XX Hepatitis B virus.

XX US2003206887-A1.

PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.

PR 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.

PR 20-MAR-2000; 2000US-00531025.

PR 09-AUG-2000; 2000US-00636385.

PR 24-OCT-2000; 2000US-00696347.

PR 08-JUN-2001; 2001US-00877478.

PR 24-OCT-2001; 2001US-0296876P.

PR 05-DEC-2001; 2001US-0335059P.

PR 20-FEB-2002; 2002US-0337055P.

PR 11-MAR-2002; 2002US-0358580P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

(MORR/) MORRISSEY D.
 PA (MCSM/) MCSMIGEN J A.
 PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswigen JA, Beigelman L;

DR WPI; 2003-901032/82.

XX New short interfering nucleic acid molecules which down-regulate
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.

XX Claim 11; Page 48; 72pp; English.

XX The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises a sense
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

SO Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCAAGCA 16
 DB 4 AAAGCCACCAAGCA 19

RESULT 14
 ADM00807
 ID ADM00807 standard; RNA; 19 BP.

AC ADM00807;

DT 20-MAY-2004 (first entry)

XX Hepatitis B virus short interfering nucleic acid (siNA) #1223.

XX Vincide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.

XX Hepatitis B virus.

XX US2003206887-A1.

XX 06-NOV-2003.

XX 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.

XX 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US0092187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSM/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 48; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterized genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 19 BP; 8 A; 8 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 0;
 QY 1 AAAGCACCACCAAGCA 16
 |||||
 Db 2 AAAGCACCACCAAGCA 17
 |||||
 RESULT 15

ADM00284
 ID ADM00284 standard; RNA; 19 BP.
 XX
 AC ADM00284;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Hepatitis B virus short interfering nucleic acid (siNA) #700.
 XX
 KW Virusidae; Hepatotrophic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.
 OS Hepatitis B virus.
 XX
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.
 XX
 XX
 PE 16-SEP-2002; 2002US-00244647.
 XX
 PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US0092187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSM/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 41; 72pp; English.
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 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal

CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 CC
 SQ Sequence 19 BP; 8 A; 7 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAAAGCA 16
 DB 1 AAAGCCACCCAAAGCA 16

RESULT 16

ID ADM00804 standard; RNA; 19 BP.

AC ADM00804;
 DT 20-MAY-2004 (first entry)
 XX Hepatitis B virus short interfering nucleic acid (siNA) #1220.
 DE Hepatitis B virus short interfering nucleic acid (siNA) #1220.
 XX
 KM siNA; hepatitis B virus; HBV; RNA interference.
 OS Hepatitis B virus.
 XX
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.
 XX
 PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00434630.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.

PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswiggen JA, Beigelman L;
 DR WPI; 2003-901032/82.

PT New short interfering nucleic acid molecules which down-regulate
 PT expression of a hepatitis B virus (HBV) or which inhibit HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX

PS Claim 11; Page 48; 72pp; English.

XX The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesising a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAAAGCA 16
 DB 3 AAAGCCACCCAAAGCA 18

RESULT 17

ID ADL99637 standard; RNA; 19 BP.

AC ADL99637;
 DT 20-MAY-2004 (first entry)
 XX Hepatitis B virus short interfering nucleic acid (siNA) #54.
 DE Hepatitis B virus short interfering nucleic acid (siNA) #54.
 XX
 KM siNA; hepatitis B virus; HBV; RNA interference.
 OS Hepatitis B virus.
 XX
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00434630.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 XX
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 41; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises a sense
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises a sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 4 C; 7 G; 0 T; 8 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCACCAGGCA 16
 19 AAAGCACCAGGCA 4
 Db 19 AAAGCACCAGGCA 4
 RESULT 18
 ADM00161/c
 ID ADM00161 standard; RNA; 19 BP.
 XX
 AC ADM00161;
 XX
 DT 20-MAY-2004 (first entry)
 XX

DE Hepatitis B virus short interfering nucleic acid (siNA) #577.
 XX
 XX V-nucleide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KM siNA; hepatitis B virus; HBV, RNA interference.
 OS
 OS Hepatitis B virus.
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 16-SEP-2002; 2002US-00244647.
 XX
 XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 XX
 DR WPI; 2003-901032/82.
 XX
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 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
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 CC comprises a sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
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 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
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CC siNA molecules of the invention.

CC Sequence 19 BP; 0 A; 3 C; 8 G; 0 T; 8 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 18 AAAGCCACCCAGGCA 3

RESULT 19
ADM00158/C
ADM00158 standard; RNA; 19 BP.

AC ADM00158;

DT 20-MAY-2004 (first entry)

DE Hepatitis B virus short interfering nucleic acid (siNA) #574.

KM Viruslike; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW siNA; hepatitis B virus; HBV; RNA interference.

OS Hepatitis B virus.

PN US2003206887-A1.

PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002US-05009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

XX (MORR/) MORRISSEY D.
PA (MCSW/) MCSWIGEN J A.
PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswigen JA, Beigelman L;

DR WPI; 2003-901032/82.

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CC comprises sequence complementary to the antisense region. The siNA
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CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
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CC infections, and for characterizing pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterized genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.

Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 17 AAAGCCACCCAGGCA 2

RESULT 20
AAQ13771/C
AAQ13771 standard; DNA; 20 BP.

XX AAQ13771;
AC
DT 25-MAR-2003 (revised)
DT 03-JAN-1992 (first entry)

DE HBV primer number 12.

XX Hepatitis B virus; ss.

OS Synthetic.

PN WO9114789-A.

PD 03-OCT-1991.

PF 28-MAR-1990; 90GB-00006924.

PR 28-MAR-1990; 90GB-00006924.

PA (UNIO) IMPERIAL COLLEGE SCI & TECHN.

PI Thomas H, Carman WF;

DR WPI; 1991-310588/42.

XX Predicting course of hepatitis B infection - by detecting viral strains
PT carrying specific mutation(s) more likely to cause fulminating
PT infections.

PS Disclosure; Page 3; 19pp; English.

XX The primer corresponds to positions 1877-1896 of HBV DNA. It is used to
CC detect the presence/absence of a pre-core variant of HB virus having the

CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with the mu-1896 mutation. See also AAQ13770-
 CC Q13773 (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 20 BP; 1 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 19 AAAGCCACCCAGGCA 4

RESULT 21
 AAQ13772/c
 ID AAQ13772 standard; DNA; 20 BP.
 XX
 AC AAQ13772;
 XX

DT 25-MAR-2003 (revised)
 PT 03-JUN-1992 (first entry)
 XX

DE HBV primer number 13.
 XX

KM Hepatitis B virus; ss.
 XX

OS Synthetic.
 XX

PN WO9114789-A.
 XX

PD 03-OCT-1991.
 XX

PF 28-MAR-1990; 90GB-00006924.
 XX

PR 28-MAR-1990; 90GB-00006924.
 XX

PA (UNLO) IMPERIAL COLLEGE SCI & TECHN.
 XX

PI Thomas H. Carman WF;
 XX

DR WPI; 1991-310588/42.
 XX

PT Predicting course of hepatitis B infection - by detecting viral strains
 PT carrying specific mutation(s) more likely to cause fulminating
 PT infections.
 XX

PS Disclosure; Page 3; 199p; English.
 XX

CC The primer corresponds to positions 1877-1896 of HBV DNA. It is used to
 CC detect the presence/absence of a pre-core variant of HB virus having the
 CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with neither mutation. See also AAQ13770-013773
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 20 BP; 0 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 19 AAAGCCACCCAGGCA 4

RESULT 22
 AAQ85970
 ID AAQ85970 standard; DNA; 20 BP.
 XX
 AC AAQ85970;
 XX

DT 31-OCT-1995 (first entry)
 XX
 DE Hepatitis B virus polypeptide coding sequence primer p205.
 XX

KM Hepatitis B virus; PCR; amplification; primer; antiviral agent; ss.
 XX

OS Synthetic.
 XX

PN JP07033797-A.
 XX

PD 03-FEB-1995.
 XX

PF 21-JUL-1993; 93JP-00180314.
 XX

PR 21-JUL-1993; 93JP-00180314.
 XX

PA (MITU) MITSUBISHI KASEI CORP.
 XX

DR WPI; 1995-110649/15.
 XX

PT Polypeptide derived from hepatitis B virus and its coding gene. - may be
 PT used for detection of HBV not detectable by conventional methods.
 XX

PS Example 2; Page 5; 7pp; Japanese.
 XX

CC Primers AAQ85967-70 were used to PCR amplify the coding sequence for a
 CC polypeptide derived from hepatitis B virus (AAQ85966). The sequence
 CC encodes a polypeptide of 134 amino acids. The DNA was isolated from
 CC patients infected with hepatitis virus which was not detected by
 CC conventional methods. The polypeptide can be used in the diagnosis of
 CC hepatitis viral diseases which cannot be detected by conventional methods
 CC and in the development of antiviral agents
 XX

SQ Sequence 20 BP; 8 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 3 AAAGCCACCCAGGCA 18

RESULT 23
 AAT70947
 ID AAT70947 standard; DNA; 20 BP.
 XX
 AC AAT70947;
 XX

DT 27-OCT-1997 (first entry)
 XX

DE HBV pre-genome element epsilon region antisense oligonucleotide.
 XX

KM HBV; hepatitis B virus; S; surface antigen; C; core; P; polymerase;
 KM antisense; replication inhibition; hepatitis; infection; diagnosis;
 KM hepatocellular carcinoma; ss.
 XX

OS Synthetic.
 XX

PN WO9703211-A1.
 XX

PD 30-JAN-1997.
 XX

PF 26-JUN-1996; 96WO-US010984.
 XX

PR 13-JUL-1995; 95US-00501968.
 XX

PA (ISIS-) ISIS PHARM INC.
 XX

PI Anderson KP, Cowbert LM;
 XX

DR WPI; 1997-119063/11.
 XX

XX New oligo:nucleotide(s) hybridisable with Hepatitis B virus RNA - used
 PT for inhibiting HBV replication and for diagnosis, treatment or prevention
 PT of HBV-associated diseases e.g. hepatitis.
 XX
 PS Claim 4, Page 16; 47pp; English.
 XX
 CC AAT70930-170969 are antisense oligonucleotides (ONs) capable of
 CC inhibiting the replication of hepatitis B virus (HBV). The ONs
 CC specifically hybridise to HBV RNA or pre-RNA which encodes a P (DNA
 CC polymerase), S (surface antigen) or C (core) gene product and/or with HBV
 CC ss RNA pre-genome elements e.g. 5' cap region, US region, epsilon region
 CC or a translation initiation site. The ONs can be used for diagnosing HBV
 CC infection, for inhibiting HBV replication and for treating or preventing
 CC a HBV associated diseases, e.g. acute, chronic or fulminant hepatitis or
 CC hepatocellular carcinoma
 CC
 SQ Sequence 20 BP; 8 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16
 RESULT 24
 ID AAQ92909 standard; cDNA; 21 BP.
 AC AAQ92909;
 XX
 DT 28-FEB-1996 (first entry)
 XX
 DE Antiviral oligonucleotide loop inhibits HBV replication.
 XX
 KM Replication; hepatitis virus; primer; DR11 region; hepatocyte; antiviral;
 KM herpes; influenza; drug; pre-S1 protein; polymerase; encapsidation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9519433-A2.
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000508.
 XX
 PR 12-JAN-1994; 94US-00181557.
 PR 08-AUG-1994; 94US-00287337.
 XX
 PA (TARG-) TARGETTECH INC.
 XX
 PI Carmichael E;
 PI
 DR WPI; 1995-263863/34.
 XX
 PT New oligo and polynucleotide(s) that inhibit viral replication -
 PT hybridise e.g. to an RNA primer or primer binding region, and their new
 PT soluble complexes, esp. for treating hepatitis B infection.
 XX
 PS Claim 20; Page 19; 31pp; English.
 XX
 CC Oligonucleotides AAQ92905-12 are used to inhibit the replication of
 CC hepatitis virus replication. This oligonucleotide binds to the cis-
 CC encapsidation signal of hepatitis B virus. The oligonucleotides are
 CC introduced into pref. hepatocytes, as soluble molecular complexes. They
 CC are used to treat hepatitis B virus infections but could also be used
 CC against e.g. Hepatitis A or C, herpes, influenza, etc. The
 CC oligonucleotides can also be used to detect the presence of the virus in
 CC a sample or to evaluate the effect of antiviral drugs
 CC

SQ Sequence 21 BP; 7 A; 10 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 6 AAAGCCACCCAGGCA 21
 RESULT 25
 ID AAT18255 standard; DNA; 21 BP.
 AC AAT18255;
 XX
 DT 17-SEP-1996 (first entry)
 XX
 DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2b.
 XX
 KM Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
 KM epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;
 KM treatment; chronic infection; modulation; translation; transcription;
 KM release; host cell; ss.
 XX
 OS Synthetic.
 XX
 PN WO9603152-A1.
 PD 08-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-US009143.
 PR 28-JUL-1994; 94US-00281106.
 XX
 PA (GEOU) UNIV GEORGETOWN.
 XX
 PI Korba BF, Gerin JL;
 PI
 DR WPI; 1996-116796/12.
 XX
 PT Single stranded oligo:nucleotide(s) for inhibiting replication of
 PT hepatitis B virus - are anti-sense to portions of the epsilon
 PT encapsidation sequence and modulate HBV function.
 XX
 PS Claim 14; Page 44; 56pp; English.
 XX
 CC The present sequence, which inhibits the replication of hepatitis B virus
 CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
 CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
 CC from the HBV genome. The 1st nucleotide of the oligonucleotide
 CC corresponds to nucleotide 1884 of the HBV ayw subtype C gene, using the
 CC numbering scheme from the sequence published by Galibert et al., Nature
 CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
 CC treat chronic HBV infection by modulating a HBV related function, e.g.
 CC translation, transcription, encapsidation, replication and release from a
 CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in
 CC the extracellular medium (VIR. DNA), intracellular viral replicative
 CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
 CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
 CC antigen protein (HBcAg), given as the EC(90) (microm, 9 days of
 CC treatment) or ND (not determined), are VIR. DNA (11.8), HBV RI (ND), HBV
 CC RNA (ND), HBsAg (>20), HBeAg (>20) and HBcAg (18.8)
 CC
 SQ Sequence 21 BP; 8 A; 10 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16

Db 6 AAAGCCACCCAGGCA 21

RESULT 26

AAAT18253
ID AAAT18253 standard; DNA; 21 BP.

AC AAAT18253;

DT 17-SEP-1996 (first entry)

DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2.

XX Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;

KM epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;

KM treatment; chronic infection; modulation; translation; transcription;

KM release; host cell; ss.

OS Synthetic.

PN MO9603152-A1.

PD 08-FEB-1996.

PF 28-JUL-1995; 95MO-US009143.

PR 28-JUL-1994; 94US-00281106.

PA (GEOU) UNIV GEORGETOWN.

PI Korba BE, Gerin JL;

DR WPI; 1996-116796/12.

PT Single stranded oligo:nucleotide(s) for inhibiting replication of

PT hepatitis B virus - are anti-sense to portions of the epsilon

PS encapsidation sequence and modulate HBV function.

XX Claim 12; Page 44; 56pp; English.

XX The present sequence, which inhibits the replication of hepatitis B virus

CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that

CC binds the epsilon encapsidation sequence of a mRNA intermediate derived

CC from the HBV genome. The 1st nucleotide of the oligonucleotide

CC corresponds to nucleotide 1879 of the HBV ayw subtype C gene, using the

CC numbering scheme from the sequence published by Galibert et al., Nature

CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to

CC treat chronic HBV infection by modulating a HBV related function, e.g.

CC translation, transcription, encapsidation, replication and release from a

CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in

CC the extracellular medium (VIR. DNA), intracellular viral replicative

CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface

CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core

CC antigen protein (HBcAg), given as the EC(90) (micromol, 9 days of

CC treatment) or ND (not determined), are VIR. DNA (15.9), HBV RI (ND), HBV

CC RNA (ND), HBeAg (>20), HBsAg (>20) and HBcAg (>20)

XX Sequence 21 BP; 8 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
1 AAAGCCACCCAGGCA 16

Db 1 AAAGCCACCCAGGCA 16

RESULT 27

AAAT70936
ID AAAT70936 standard; DNA; 21 BP.

AC AAAT70936;

XX 27-OCT-1997 (first entry)

DE HBV core gene antisense oligonucleotide.

XX HBV; hepatitis B virus; S; surface antigen; C; core; P; polymerase;

KM antisense; replication inhibition; hepatitis; infection; diagnosis;

XX hepatocellular carcinoma; ss.

OS Synthetic.

PN MO9703211-A1.

PD 30-JAN-1997.

PF 26-JUN-1996; 96MO-US010984.

PR 13-JUL-1995; 95US-00501968.

PA (ISIS-) ISIS PHARM INC.

PI Anderson KP, Cowser LM;

DR WPI; 1997-119063/11.

PT New oligo:nucleotide(s) hybridizable with Hepatitis B virus RNA - used

PT for inhibiting HBV replication and for diagnosis, treatment or prevention

PS of HBV-associated diseases e.g. hepatitis.

XX Example 1; Page 16; 47pp; English.

CC AAAT70930-T70969 are antisense oligonucleotides (ONs) capable of

CC inhibiting the replication of hepatitis B virus (HBV). The ONs

CC specifically hybridize to HBV RNA or pre-RNA which encodes a P (DNA

CC polymerase), S (surface antigen) or C (core) gene product and/or with HBV

CC ss RNA pre-genome elements e.g. a 5' cap region, US region, epsilon

CC region or a translation initiation site. The ONs can be used for

CC diagnosing HBV infection, for inhibiting HBV replication and for treating

CC or preventing a HBV associated disease, e.g. acute, chronic or fulminant

CC hepatitis or hepatocellular carcinoma

XX Sequence 21 BP; 8 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

QY 1 AAAGCCACCCAGGCA 16
3 AAAGCCACCCAGGCA 18

Db 3 AAAGCCACCCAGGCA 18

ADAL3842/c

ADAL3842 standard; RNA; 21 BP.

ADAL3842;

ADAL3842;

ADAL3842;

ADAL3842;

ADAL3842;

ADAL3842;

ADAL3842;

ADAL3842;

XX OS Synthetic.
 XX PN WO2003070918-A2.
 XX XX 28-AUG-2003.
 XX PD 20-FEB-2003; 2003WO-US005346.
 XX PF 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PR 15-JAN-2003; 2003US-0440129P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P,
 XX PI Morrissey D, Fossnaugh K, Mokler V, Jamison S,
 XX DR WPI; 2003-689785/65.
 XX XX
 XX PT New short interfering nucleic acid containing no ribonucleotides, useful
 XX PT e.g. for treating viral infection, downregulates expression of target
 XX PT gene or RNA.
 XX PS Example 4; Page 137; 204pp; English.
 XX XX
 XX CC The present invention describes a double-stranded short interfering
 XX CC nucleic acid (siNA) that downregulates expression of a target gene, where
 XX CC the siNA molecule comprises no ribonucleotides and each strand of the
 XX CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)
 XX CC a siNA molecule that inhibits expression of target RNA; (2) a siNA
 XX CC molecule that inhibits replication of a virus and optionally does not
 XX CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule
 XX CC that inhibits expression of a target gene and does not require presence
 XX CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
 XX CC expression of a target gene by mediating RNA interference; and (5) a
 XX CC method for modulating expression of a gene in a cell using siNA
 XX CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,
 XX CC anti-inflammatory, plant antiviral, vasotropic, neuroprotective,
 XX CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotoxic
 XX CC and endocrine activities. The siNA's are useful for downregulating
 XX CC expression of target genes, inhibiting expression of target RNA, and
 XX CC inhibiting replication of a virus. siNA molecules can be used: (a) for
 XX CC therapy of any disorder that responds to modulation of gene expression,
 XX CC especially animal and plant viral infections, specifically hepatitis B or
 XX CC C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory
 XX CC syncytial or influenza viruses, and also many other diseases such as
 XX CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
 XX CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
 XX CC endocrine or reproductive diseases; and (b) for diagnosis, target
 XX CC validation, genomic discovery, genetic engineering, pharmacogenomics and
 XX CC analysis of gene function. Chemical modification of siNA molecules
 XX CC improves interfering activity; stability; cellular uptake; binding
 XX CC affinity and/or mediates increased polymerase activity. siNA may be
 XX CC designed to target many related genes containing a conserved sequence.
 XX CC The present sequence represents a siNA oligonucleotide sequence, which is
 XX CC used in the exemplification of the present invention.
 XX XX
 XX SQ Sequence 21 BP; 1 A; 4 C; 8 G; 2 T; 6 U; 0 Other;
 XX XX
 XX Best Local Match 100.0%; Score 16; DB 9; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 9.5;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCCAAGGCA 16
 Db 21 AAAGCCACCCCAAGGCA 6

RESULT 29
 ADM00924/C
 ID ADM00924 standard; RNA, 21 BP.
 XX AC ADM00924;
 XX XX
 XX DT 20-MAY-2004 (first entry)
 XX XX
 XX DE Hepatitis B virus short interfering nucleic acid (siNA) #1340.
 XX XX
 XX KW Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 XX KW siNA; hepatitis B virus; HBV; RNA interference.
 XX OS Hepatitis B virus.
 XX XX
 XX EN US2003206887-A1.
 XX PD 06-NOV-2003.
 XX XX
 XX PF 16-SEP-2002; 2002US-00244647.
 XX XX
 XX PR 14-MAY-1992; 92US-00882712.
 XX PR 07-FEB-1994; 94US-00193627.
 XX PR 08-NOV-1999; 99US-00436430.
 XX PR 20-MAR-2000; 2000US-00531025.
 XX PR 09-AUG-2000; 2000US-00636385.
 XX PR 24-OCT-2000; 2000US-00696347.
 XX PR 08-JUN-2001; 2001US-00877478.
 XX PR 08-JUN-2001; 2001US-0296876P.
 XX PR 24-OCT-2001; 2001US-0335059P.
 XX PR 05-DEC-2001; 2001US-0337055P.
 XX PR 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 26-MAR-2002; 2002WO-US00918P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX XX
 XX PA (MORE/) MORRISSEY D.
 XX PA (MCSW/) MCSWIGGEN J A.
 XX PA (BEIG/) BEIGELMAN L J.
 XX XX
 XX PI Morrissey D, McSwiggen JA, Beigelman L,
 XX PI WPI; 2003-901032/82.
 XX XX
 XX PT New short interfering nucleic acid molecules which down-regulates
 XX PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 XX PT replication, useful for treating human HBV infections or for
 XX PT characterizing gene function.
 XX PT
 XX PS Claim 11; Page 51; 72pp; English.
 XX XX
 XX CC The invention relates to a short interfering nucleic acid (siNA) molecule
 XX CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 XX CC interference or that inhibits HBV replication. Also disclosed are the
 XX CC following: (i) a method of modulating the expression of a HBV gene in a
 XX CC tissue explant; (ii) a method of generating a library of siNA constructs
 XX CC having predetermined complexity; (iii) a cell containing one or more siNA
 XX CC molecules; (iv) a kit containing a siNA molecule which can be used to
 XX CC modulate the expression of a HBV target gene in a cell, tissue or
 XX CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 XX CC molecule is adapted for use to treat HBV infection, and comprises a sense
 XX CC and an antisense region, where the antisense region comprises sequence
 XX CC complementary to an RNA sequence encoding HBV and the sense region
 XX CC comprises sequence complementary to the antisense region. The siNA
 XX CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 XX CC comprises the sense region and the second fragment comprises the
 XX CC antisense region of the siNA molecule, where sense region and the
 XX CC antisense region comprise separate oligonucleotides, and are covalently
 XX CC connected via a linker molecule. The linker molecule is a polynucleotide
 XX CC linker or a non-nucleotide linker. The sense region comprises a 3'-

CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

XX
 SQ Sequence 21 BP; 1 A; 4 C; 8 G; 2 T; 6 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 DB 21 AAAGCCACCCAGGCA 6

RESULT 30
 ID AAQ13770/c
 XX AAQ13770 standard; DNA; 23 BP.

AC AAQ13770;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)
 XX
 DE HBV primer number 11.

XX Hepatitis B virus; ss.

XX Synthetic.

XX MO9114789-A.

XX PD 03-OCT-1991.

XX PF 28-MAR-1990; 90GB-00006924.

XX PR 28-MAR-1990; 90GB-00006924.

XX PA (UNLO) IMPERIAL COLLEGE SCI & TECHN.

XX PI Thomas H. Carman WF;

XX DR WPI; 1991-310588/42.

XX PT Predicting course of hepatitis B infection - by detecting viral strains
 PT carrying specific mutation(s) more likely to cause fulminating
 PT infections.

XX PS Disclosure; Page 3; 19pp; English.

XX CC The primer corresponds to positions 1877-1899 of HBV DNA. It is used to
 CC detect the presence/absence of a pre-core variant of HB virus having the
 CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with both the mutations. See also AAQ13771-Q13773
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 23 BP; 2 A; 4 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 DB 19 AAAGCCACCCAGGCA 4

RESULT 31
 ID AAT03266/c
 XX AAT03266 standard; DNA; 23 BP.

XX AC AAT03266;

XX DT 02-APR-1996 (first entry)

XX DE Hepatitis B virus (HBV) sense primer OAL41.

XX KW Polymerase chain reaction; PCR; primer; amplify; hepatitis B virus; HBV;
 KW prec; S gene; diagnosis; ss.

XX OS Synthetic.

XX PN JP07203972-A.

XX PD 08-AUG-1995.

XX PE 07-JAN-1994; 94JP-00000515.

XX PR 07-JAN-1994; 94JP-00000515.

XX PA (SAGA) OTSUKA PHARM CO LTD.

XX DR WPI; 1995-307167/40.

XX PT Hepatitis B virus DNA fragment contg. S gene region and mutant prec
 PT region - useful for simultaneous detection of mutant and complete HBV DNA
 PT for diagnosis of hepatitis B.

XX PS Example 1; Col 7; 10pp; Japanese.

XX CC The sequences represented by AAT03266-T03272 are amplification primers
 CC for Hepatitis B virus DNA fragments containing the S gene region and the
 CC mutant prec region. This sequence corresponds to nucleotides 1748-1770 of
 CC HBV-DNA. The mutant prec region produces no HBe antigen and contains a
 CC point mutation (G83 to A83). The DNA fragments can be used for a
 CC simultaneous determination of a mutant HBV-DNA and a total HBV-DNA. This
 CC can be used to diagnose hepatitis B

XX SQ Sequence 23 BP; 3 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 DB 22 AAAGCCACCCAGGCA 7

RESULT 32
 ID AAQ81424/c
 XX AAQ81424 standard; DNA; 23 BP.

XX AC AAQ81424;

XX DT 25-MAR-2003 (revised)

XX DT 13-AUG-1995 (first entry)

XX DE HBV hybridization probe.

XX KW HBV; hepatitis B virus; hybridization; probe; detection; PCR;
 KW polymerase chain reaction; LCR; ligase chain reaction; ss.

XX OS Synthetic.

XX PN WO9502690-A1.

XX PD 26-JAN-1995.

PF 08-JUL-1994; 94MO-US007684.
XX
PR 13-JUL-1993; 93US-00090755.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Spies U;
XX
DR WPI; 1995-067334/09.
XX
PT Novel composition containing ligation incompetent upstream and downstream
XX probes - for the detection of hepatitis B virus.
PS Disclosure; Page 45; 70pp; English.
XX
CC Probes given in AAQ81412-31 and AAQ81437-44 are used to detect hepatitis
CC B virus (HBV) in test samples. The probes, which include ligation
CC incompetent upstream and downstream probes that can be corrected by a gap
CC -fill or exo format, and which can be used in PCR and LCR protocols,
CC hybridize to target sequences of HBV, selected from those given in
CC AAQ81432-36. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 23 BP; 2 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGCCACCCCAAGGCA 16
Db 23 AAAGCCACCCCAAGGCA 8

RESULT 33
AAD19005/c
ID AAD19005 standard; DNA; 23 BP.
AC AAD19005;
XX
DT 18-DEC-2001 (first entry)
XX
DE Hepatitis B virus (HBV) precore DNA amplifying forward PCR primer #5.
XX
KM Hepatitis B virus; HBV; bacterial infection; fungi; protozoa; PCR primer;
KM amplification; blood-borne pathogen; sexually transmitted disease;
KM respiratory disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001MO-US008110.
XX
PR 14-MAR-2000; 2000US-0189344P.
XX
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, Mccue KF;
XX WPI; 2001-611396/70.
XX
DR Simultaneous detection of biological entities such as bacteria, fungi and
XX viruses by specific nucleic acid amplification.
PT Disclosure; Page 31; 55pp; English.
XX

CC The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a

CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC cause by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (staphylococcus, pneumococcus,
CC gonococcus, haemophilus, bacitoides, escherichia or salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (aspergillus fumigatus, blastomycosis,
CC dermatitis, candida albicans) or protozoa (Entamoeba histolytica). The
CC present sequence is a PCR primer used for amplifying Hepatitis B Virus
CC (HBV) precore DNA
XX
SQ Sequence 23 BP; 2 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGCCACCCCAAGGCA 16
Db 23 AAAGCCACCCCAAGGCA 8

RESULT 34
ADM00880/c
ID ADM00880 standard; RNA; 23 BP.
XX
AC ADM00880;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #1296.
XX
KM Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KM siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206887-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-0051025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 24-OCT-2001; 2001US-0296876P.
PR 05-DEC-2001; 2001US-0335059P.
PR 20-FEB-2002; 2002US-0337055P.
PR 11-MAR-2002; 2002US-0358580P.
PR 26-MAR-2002; 2002MO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
XX
XX (MORR/) MORRISSEY D.
XX (MCSW/) MCSWIGEN J A.
XX (BEIG/) BEIGELMAN L.
XX
PI Morrissey D, Mcswiggen JA, Beigelman L;
XX WPI; 2003-901032/82.
XX
DR New short interfering nucleic acid molecules which down-regulates
XX expression of a hepatitis B virus (HBV) or which inhibits HBV

PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 XX
 PS Claim 11; Page 51; 72pp; English.
 CC
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-terminal
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 23 BP; 2 A; 5 C; 8 G; 0 T; 8 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 11; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 23 AAAGCCACCCAGGCA 8
 XX
 RESULT 35
 ID AAV29303 standard; DNA; 30 BP.
 XX
 AC AAV29303;
 XX
 DT 27-AUG-2003 (revised)
 DT 29-JUL-1998 (first entry)
 XX
 DE Hepatitis B virus (HBV) core fragment DNA amplifying primer 3.
 XX
 KM Hepatitis B virus; HBV; vaccine; treatment; viral infection;
 KM hepatitis infection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO9811916-A1.
 XX
 PD 26-MAR-1998.
 XX
 PF 18-SEP-1997; 97MO-US016541.
 XX
 PR 18-SEP-1996; 96US-0026313P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX

PI Shih C, Yuan T;
 XX
 DR WPL; 1998-217032/19.
 XX
 PT Defective interfering virus particle that occurs naturally in infection -
 PT used in protective vaccines and for treating viral, specifically
 PT hepatitis B, infections.
 XX
 PS Example 1; Page 23; 84pp; English.
 CC
 CC This primer is used for the PCR amplification of the Hepatitis B virus
 CC (HBV) DNA. This is used for the detection of a core deleted variant found
 CC in HBV infections. A defective, interfering virus particle that occurs
 CC naturally in a human infection has been identified. The invention
 CC provides a vector comprising a DNA sequence encoding the defective virus
 CC particle and origin of replication and a promoter/enhancer element. Host
 CC cells transformed with this vector can produce this defective virus
 CC particle which is useful in vaccines (of live virus or subunit types),
 CC particularly against HBV infection, including use in babies born to
 CC mothers who are not HBV carriers (particularly administered together with
 CC HBV-specific immunoglobulin). The defective interfering virus particle
 CC can also be used to treat infections, especially fulminant, chronic or
 CC acute hepatitis. Since the defective particle is almost identical to
 CC fully infectious virus, it should produce a stronger, more effective and
 CC longer-lasting protection against HBV than known subunit vaccines based
 CC on surface antigen only, with a lower failure rate. (Updated on 27-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 30 BP; 5 A; 5 C; 10 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 30 AAAGCCACCCAGGCA 15
 XX
 RESULT 36
 ID AAS14628 standard; DNA; 32 BP.
 XX
 AC AAS14628;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE NASBA molecular beacon probe MB WT 1.
 XX
 KM NASBA; nucleic acid sequence based amplification; ss; probe;
 KM anchor sequence; anti-viral; hepatitis B virus; HBV; HBV infection;
 KM isothermal continuous transcription based amplification; WT 1.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Fluorescein labelled"
 FT modified_base 32
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "DABCYL (not defined) labelled as a quencher"
 XX
 PN WO200164959-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001MO-EP002143.
 XX
 PR 02-MAR-2000; 2000EP-00200737.
 XX

PA (ALKU) AKZO NOBEL NV.
 XX
 PI Goudamit J, Yates SC, Penning MT, Van De Weijer LHM;
 XX
 DR WPI, 2001-602572/68.
 XX
 PT Monitoring anti-viral therapy, where hepatitis B virus (HBV) mRNA is
 PT detected, useful for monitoring the efficacy of HBV treatment, by
 PT amplifying a target nucleic acid in a sample obtained from a subject
 XX suspected of HBV infection.
 PS
 XX Example 6; Page 12; 42pp; English.
 CC The invention relates to monitoring anti-viral therapy, where hepatitis B
 CC virus (HBV) mRNA is detected, comprising amplifying a target nucleic acid
 CC sequence in a sample, which is obtained from an individual suspected of
 CC HBV infection, using at least one oligonucleotide primer and
 CC amplification reagents. The amplification method is preferably NASBA
 CC (nucleic acid sequence based amplification) which is an isothermal
 CC continuous transcription based amplification method. The method is useful
 CC for monitoring anti-viral therapy, where HBV is detected. In particular,
 CC the method is useful for monitoring the efficacy of the treatment. Prior
 CC methods are either based on immunologic markers or the detection of the
 CC HBV DNA in virus particles. The present method actually directly measures
 CC the replication of the virus and immediately indicates the emergence of
 CC resistant virus strains. The present method also provides insight into
 CC how to interpret the results in order to predict the outcome of the
 CC therapy. Thus, a more efficient therapy can be given to the patient
 CC concerned. The present sequence is a NASBA molecular beacon probe for use
 CC in the method of the invention
 CC
 SQ Sequence 32 BP; 2 A; 7 C; 14 G; 9 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAGCCACCCCAAGCA 16
 Db 22 AAAGCCACCCCAAGCA 7
 RESULT 37
 AAT71784/c
 ID AAT71784 standard; DNA; 44 BP.
 XX
 AC AAT71784;
 XX
 DT 29-AUG-1997 (first entry)
 XX
 DE Hepatitis B virus precore antigen target sequence mutant.
 XX
 KM HBV, ligase chain reaction; internal standard; amplification; ds.
 XX
 OS Hepatitis B virus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_difference 19 /*tag= a
 FT /*tag= b
 FT misc_difference 21 /note= "G in wild-type"
 FT /*tag= b
 FT /note= "G in wild-type"
 XX
 PN WO9640996-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US008429.
 XX
 PR 07-JUN-1995; 95US-00480220.
 XX

PA (ABBO) ABBOTT LAB.
 XX
 PI Birkenmeyer L, Mushahwar IK;
 XX
 DR WPI, 1997-052367/05.
 XX
 PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
 PT virus - can distinguish wild-type and mutant DNA types.
 XX
 PS
 XX Claim 13; Page 29; 40pp; English.
 CC A novel method has been produced for detecting the amount of a target
 CC nucleic acid sequence which may be present in a test sample. It involves
 CC contacting the test sample with means for performing a nucleic acid
 CC amplification reaction; and determining the ratio of target amplification
 CC products to internal standard amplification products present in the
 CC sample. The present sequence represents a target sequence from hepatitis
 CC B virus (HBV) precore antigen (mutant). The method can be used for
 CC distinguishing between two different nucleic acid sequences present in a
 CC sample, e.g. wild-type and mutant. The compositions can be used for
 CC quantitatively detecting the DNA of HBV
 CC
 SQ Sequence 44 BP; 10 A; 8 C; 12 G; 14 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAGCCACCCCAAGCA 16
 Db 18 AAAGCCACCCCAAGCA 3
 RESULT 38
 AAT71783/c
 ID AAT71783 standard; DNA; 44 BP.
 XX
 AC AAT71783;
 XX
 DT 29-AUG-1997 (first entry)
 XX
 DE Hepatitis B virus precore antigen target sequence wild-type.
 XX
 KM HBV, ligase chain reaction; internal standard; amplification; ds.
 XX
 OS Hepatitis B virus.
 XX
 PN WO9640996-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US008429.
 XX
 PR 07-JUN-1995; 95US-00480220.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Birkenmeyer L, Mushahwar IK;
 XX
 DR WPI, 1997-052367/05.
 XX
 PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
 PT virus - can distinguish wild-type and mutant DNA types.
 XX
 PS
 XX Claim 13; Page 29; 40pp; English.
 CC A novel method has been produced for detecting the amount of a target
 CC nucleic acid sequence which may be present in a test sample. It involves
 CC contacting the test sample with means for performing a nucleic acid
 CC amplification reaction; and determining the ratio of target amplification
 CC products to internal standard amplification products present in the
 CC sample. The present sequence represents a target sequence from hepatitis
 CC B virus (HBV) precore antigen (wild-type). The method can be used for

CC distinguishing between two different nucleic acid sequences present in a
 CC sample e.g. wild-type and mutant. The compositions can be used for
 CC quantitatively detecting the DNA of HBV
 XX

SO Sequence 44 BP; 8 A; 8 C; 14 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGCCACCCAGGCA 16
 DB 18 AAGGCCACCCAGGCA 3

RESULT 39
 ID ABK14698/c
 ABK14698 standard; RNA; 48 BP.

AC ABK14698;
 DT 08-MAY-2002 (first entry)

XX HBV encapsidation signal target sequence #1.

KW Encapsidation signal; epsilonRNA; virucide; hepatotropic;
 KW antiinflammatory; hepatitis B virus; infection; chicken pox;
 KW 1,3,5-triazine derivative; DNA virus; RNA virus; gastroenteritis;
 KW infectious mononucleosis; smallpox; allergic rash; aseptic meningitis;
 KW influenza; acquired immune deficiency syndrome; AIDS; measles; ss.
 XX Hepatitis B virus.

FT Key Location/Qualifiers
 FT misc_binding 6..9

FT /tag= a
 FT /bound_moiety= "Binds nucleotides 48-45 of the present
 FT sequence"
 FT 16..20

FT /tag= b
 FT /bound_moiety= "Binds nucleotides 44-40 of the present
 FT sequence"
 FT 22..37

FT /tag= d
 FT 40..44
 FT /tag= e
 FT /bound_moiety= "Binds nucleotides 20-16 of the present
 FT sequence"
 FT 45..48

FT /tag= f
 FT /bound_moiety= "Binds nucleotides 9-6 of the present
 FT sequence"

PN US635339-B1.

PD 01-JAN-2002.

PF 13-JAN-1999; 99US-00229703.

PR 13-JAN-1998; 98US-0006430.

PR 13-JAN-1998; 98US-0113656P.

PA (SCRI-) SCRIPTGEN PHARM INC.

PI Arenas JE, Cload ST, Fleming ES, Xiang YB,

PT WPI; 2000-022911/02.
 PT Pharmaceutical formulations for treating HBV and microbial infections and
 PT detecting target nucleic acids.

PS Disclosure; Fig 255B, 11app; English.

CC This invention relates to a novel method for the treatment or prevention
 CC of viral infection such as hepatitis B virus infection in a patient. The
 CC method involves administering substituted 1,3,5-triazine derivatives or
 CC their salts to the patient. These triazine derivatives bind to and
 CC inhibit functional nucleic acids and as such may be used to treat many
 CC DNA and RNA viruses. The method of the invention may be used as a
 CC Hepatitis B virus (HBV) replication inhibitor and is useful for the
 CC treatment or prevention of viral infection, such as hepatitis B virus
 CC infection, gastroenteritis, chicken pox, infectious mononucleosis,
 CC smallpox, allergic rash, aseptic meningitis, influenza, acquired immune
 CC deficiency syndrome (AIDS), measles and many other diseases listed in the
 CC specification. The methods of the invention can also be used for treating
 CC diseases associated with deoxyribonucleic acid and ribonucleic acid, for
 CC detection and/or purification of nucleic acids. The present sequence
 CC represents a target sequence used in an example of the method of the
 CC invention comprising a region of the HBV encapsidation signal
 CC (epsilonRNA). This sequence is important for the encapsidation of the
 CC pregenome into virus and is also thought to play a role in activation of
 CC the HBV encoded polymerase

SO Sequence 48 BP; 8 A; 12 C; 15 G; 0 T; 13 U; 0 Other;

Query Match 100.0%; Score 16; DB 3; Length 48;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGCCACCCAGGCA 16
 DB 45 AAGGCCACCCAGGCA 30

RESULT 40
 ID ABK14696/c
 ABK14696 standard; RNA; 48 BP.

AC ABK14696;

DT 08-MAY-2002 (first entry)

XX RNA target region comprising HBV encapsidation signal.

KW Encapsidation signal; epsilonRNA; virucide; hepatotropic;
 KW antiinflammatory; hepatitis B virus; infection; chicken pox;
 KW 1,3,5-triazine derivative; DNA virus; RNA virus; gastroenteritis;
 KW infectious mononucleosis; smallpox; allergic rash; aseptic meningitis;
 KW influenza; acquired immune deficiency syndrome; AIDS; measles; ss.
 XX Hepatitis B virus.

FT Key Location/Qualifiers
 FT misc_binding 6..9

FT /tag= a
 FT /bound_moiety= "Binds nucleotides 48-45 of the present
 FT sequence"
 FT 16..20

FT /tag= b
 FT /bound_moiety= "Binds nucleotides 44-40 of the present
 FT sequence"
 FT 22..26

FT /tag= c
 FT /bound_moiety= "Binds nucleotides 38-33 of the present
 FT sequence"
 FT 33..38

FT /tag= d
 FT /bound_moiety= "Binds nucleotides 26-22 of the present
 FT sequence"
 FT 40..44

FT /tag= e
 FT /bound_moiety= "Binds nucleotides 20-16 of the present
 FT sequence"
 FT 45..48

FT /tag= f
 FT /bound_moiety= "Binds nucleotides 9-6 of the present
 FT sequence"

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FT      sequence "
XX      US6335339-B1.
PN      01-JAN-2002.
XX      13-JAN-1999; 99US-00229703.
XX      13-JAN-1998; 98US-00006430.
PR      13-JAN-1998; 98US-0113656P.
XX      (SCRI-) SCRIPGEN PHARM INC.
XX      Arenas JE, Cload ST, Fleming ES, Xiang YB;
PI      WPI; 2000-022911/02.
DR      Pharmaceutical formulations for treating HBV and microbial infections and
XX      detecting target nucleic acids.
PT      Example 2; Fig 258B; 114pp; English.
XX      This invention relates to a novel method for the treatment or prevention
XX      of viral infection such as hepatitis B virus infection in a patient. The
XX      method involves administering substituted 1,3,5-triazine derivatives or
XX      their salts to the patient. These triazine derivatives bind to and
XX      inhibit functional nucleic acids and as such may be used to treat many
XX      DNA and RNA viruses. The method of the invention may be used as a
XX      Hepatitis B virus (HBV) replication inhibitor and is useful for the
XX      treatment or prevention of viral infection, such as hepatitis B virus
XX      infection, gastroenteritis, chicken pox, infectious mononucleosis,
XX      smallpox, allergic rash, aseptic meningitis, influenza, acquired immune
XX      deficiency syndrome (AIDS), measles and many other diseases listed in the
XX      specification. The methods of the invention can also be used for treating
XX      diseases associated with deoxyribonucleic acid and ribonucleic acid, for
XX      detection and/or purification of nucleic acids. The present sequence
XX      represents a target sequence used in an example of the method of the
XX      invention comprising the HBV encapsidation signal (EpsilonRNA). This
XX      sequence is important for the encapsidation of the pregenome into virus
XX      and is also thought to play a role in activation of the HBV encoded
XX      polymerase
SQ      Sequence 48 BP; 8 A; 12 C; 15 G; 0 T; 13 U; 0 Other;
      Query Match 100.0%; Score 16; DB 3; Length 48;
      Best Local Similarity 100.0%; Pred. No. 9.4;
      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AAAGCCACCCAGGCA 16
      |||||
Db      45 AAAGCCACCCAGGCA 30

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SUMMARIES

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2	16	100.0	16	4	US-09-155-885A-41
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4	16	100.0	18	1	US-08-480-220A-22
5	16	100.0	18	2	US-08-864-404-22
6	16	100.0	18	4	US-09-155-885A-49
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9	16	100.0	19	2	US-08-864-404-21
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13	16	100.0	21	1	US-08-281-106-45
14	16	100.0	21	1	US-08-281-106-47
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16	16	100.0	21	4	US-08-501-968-7
17	16	100.0	21	4	US-09-155-885A-45
18	16	100.0	21	4	US-09-155-885A-47
19	16	100.0	21	5	PCT-US95-00508-5
20	16	100.0	21	5	PCT-US96-10984-7
21	16	100.0	23	1	US-08-758-626-13
22	16	100.0	23	5	PCT-US94-07684-13
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24	16	100.0	44	1	US-08-480-220A-20
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26	16	100.0	44	2	US-08-864-404-20
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C 28	16	100.0	50	5	PCT-US94-07684-25	Sequence 25, Appl
C 29	16	100.0	61	4	US-08-890-735C-3	Sequence 3, Appl
C 30	16	100.0	69	1	US-08-098-113-10	Sequence 10, Appl
C 31	16	100.0	69	5	PCT-US97-01188-10	Sequence 12, Appl
C 32	16	100.0	72	2	US-08-687-404-12	Sequence 9, Appl
C 33	16	100.0	81	1	US-08-287-337A-9	Sequence 8, Appl
C 34	16	100.0	114	3	US-08-075-520A-8	Sequence 11, Appl
C 35	16	100.0	291	3	US-08-075-520A-11	Sequence 16, Appl
C 36	16	100.0	390	3	US-08-075-520A-16	Sequence 2, Appl
C 37	16	100.0	477	3	US-08-445-585-2	Sequence 4, Appl
C 38	16	100.0	534	3	US-08-075-520A-4	Sequence 5, Appl
C 39	16	100.0	544	3	US-08-075-520A-5	Sequence 35, Appl
C 40	16	100.0	558	3	US-08-075-520A-35	Sequence 56, Appl
C 41	16	100.0	655	3	US-08-483-111-56	Sequence 1, Appl
C 42	16	100.0	655	5	PCT-US93-01009-56	Sequence 1, Appl
C 43	16	100.0	909	3	US-09-243-282-1	Sequence 4, Appl
C 44	16	100.0	2348	3	US-08-480-173A-42	Sequence 42, Appl
C 45	16	100.0	2348	3	US-08-484-408A-42	Sequence 42, Appl
C 46	16	100.0	3161	4	US-09-155-885A-301	Sequence 301, Appl
C 47	16	100.0	3182	4	US-08-890-735C-1	Sequence 1, Appl
C 48	16	100.0	3182	4	US-10-104-966-14	Sequence 14, Appl
C 49	16	100.0	3182	4	US-09-155-885A-302	Sequence 302, Appl
C 50	16	100.0	3182	4	US-09-155-885A-303	Sequence 303, Appl
C 51	16	100.0	3182	4	US-09-155-885A-304	Sequence 304, Appl
C 52	16	100.0	3182	4	US-09-155-885A-305	Sequence 305, Appl
C 53	16	100.0	3182	4	US-09-155-885A-306	Sequence 306, Appl
C 54	16	100.0	3182	4	US-09-155-885A-307	Sequence 307, Appl
C 55	16	100.0	3182	4	US-09-155-885A-308	Sequence 308, Appl
C 56	16	100.0	3188	4	US-09-155-885A-293	Sequence 293, Appl
C 57	16	100.0	3200	4	US-09-155-885A-280	Sequence 280, Appl
C 58	16	100.0	3212	4	US-09-155-885A-298	Sequence 298, Appl
C 59	16	100.0	3212	4	US-09-155-885A-309	Sequence 309, Appl
C 60	16	100.0	3212	4	US-09-155-885A-288	Sequence 288, Appl
C 61	16	100.0	3213	4	US-09-155-885A-289	Sequence 289, Appl
C 62	16	100.0	3213	4	US-09-155-885A-289	Sequence 289, Appl
C 63	16	100.0	3214	4	US-09-155-885A-294	Sequence 294, Appl
C 64	16	100.0	3215	4	US-09-719-528A-1	Sequence 1, Appl
C 65	16	100.0	3215	4	US-09-155-885A-284	Sequence 284, Appl
C 66	16	100.0	3215	4	US-09-155-885A-285	Sequence 285, Appl
C 67	16	100.0	3215	4	US-09-155-885A-286	Sequence 286, Appl
C 68	16	100.0	3215	4	US-09-155-885A-287	Sequence 287, Appl
C 69	16	100.0	3215	4	US-09-155-885A-290	Sequence 290, Appl
C 70	16	100.0	3215	4	US-09-155-885A-291	Sequence 291, Appl
C 71	16	100.0	3215	4	US-09-155-885A-292	Sequence 292, Appl
C 72	16	100.0	3215	4	US-09-155-885A-295	Sequence 295, Appl
C 73	16	100.0	3215	4	US-09-155-885A-299	Sequence 299, Appl
C 74	16	100.0	3215	4	US-09-155-885A-300	Sequence 300, Appl
C 75	16	100.0	3215	4	US-09-155-885A-311	Sequence 311, Appl
C 76	16	100.0	3215	4	US-09-155-885A-312	Sequence 312, Appl
C 77	16	100.0	3215	4	US-09-155-885A-313	Sequence 313, Appl
C 78	16	100.0	3220	6	US-10-209-264-1	Sequence 1, Appl
C 79	16	100.0	3220	6	5196194-11	Patent No. 5196194
C 80	16	100.0	3220	6	5196194-15	Patent No. 5196194
C 81	16	100.0	3220	6	5196194-11	Patent No. 5196194
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C 83	16	100.0	3221	2	US-09-155-885A-279	Sequence 279, Appl
C 84	16	100.0	3221	4	US-09-155-885A-281	Sequence 281, Appl
C 85	16	100.0	3221	4	US-09-155-885A-282	Sequence 282, Appl
C 86	16	100.0	3221	4	US-08-952-674-1	Sequence 1, Appl
C 87	16	100.0	4421	4	US-08-799-569-1	Sequence 1, Appl
C 88	16	100.0	5618	3	US-08-570-546-1	Sequence 1, Appl
C 89	16	100.0	5618	3	US-09-146-072A-1	Sequence 1, Appl
C 90	16	100.0	5618	4	US-09-155-885A-281	Sequence 1, Appl
C 91	16	100.0	5639	3	US-09-175-590A-1	Sequence 1, Appl
C 92	16	100.0	6371	2	US-08-715-808-5	Sequence 5, Appl
C 93	16	100.0	6371	2	US-08-715-808-12	Sequence 12, Appl
C 94	16	100.0	6375	2	US-08-715-808-14	Sequence 14, Appl
C 95	16	100.0	9325	2	US-08-715-808-1	Sequence 1, Appl
C 96	16	100.0	9542	3	US-08-968-885A-9	Sequence 9, Appl
C 97	16	100.0	9859	2	US-08-715-808-6	Sequence 6, Appl
C 98	16	93.8	16	2	US-08-501-968-37	Sequence 37, Appl
C 99	16	93.8	16	5	PCT-US96-10984-37	Sequence 19, Appl
C 100	15	93.8	20	2	US-08-501-968-19	

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C 102	15	93.8	3215	4	US-09-155-885A-296	Sequence 296, App	C 175	13	81.2	601	4	US-09-949-016-160988	Sequence 160988,
C 103	15	93.8	3215	4	US-09-155-885A-297	Sequence 297, App	C 176	13	81.2	601	4	US-09-949-016-164584	Sequence 164584,
C 104	14	87.5	18	2	US-08-501-968-28	Sequence 28, Appl	C 177	13	81.2	612	4	US-09-107-433-1970	Sequence 1970, Ap
C 105	14	87.5	18	2	PCT-US96-10984-28	Sequence 28, Appl	C 178	13	81.2	653	3	US-08-961-527-358	Sequence 358, App
C 106	14	87.5	20	5	US-08-468-352-13	Sequence 13, Appl	C 179	13	81.2	663	4	US-09-583-110-948	Sequence 948, App
C 107	14	87.5	601	4	US-09-949-016-91519	Sequence 91519, A	C 180	13	81.2	699	4	US-09-248-796A-282	Sequence 2822, Ap
C 108	14	87.5	601	4	US-09-949-016-91520	Sequence 91520, A	C 181	13	81.2	978	4	US-09-949-016-4020	Sequence 4020, Ap
C 109	14	87.5	601	4	US-09-949-016-91520	Sequence 91520, A	C 182	13	81.2	1184	4	US-09-107-433-2582	Sequence 2582, Ap
C 110	14	87.5	601	4	US-09-949-016-124541	Sequence 124541, A	C 183	13	81.2	1248	4	US-09-583-110-1589	Sequence 2728, Ap
C 111	14	87.5	601	4	US-09-949-016-14634	Sequence 14634, A	C 184	13	81.2	1248	4	US-09-583-110-1589	Sequence 1589, Ap
C 112	14	87.5	601	4	US-09-949-016-157123	Sequence 157123, A	C 185	13	81.2	1338	4	US-09-949-016-4189	Sequence 4189, Ap
C 113	14	87.5	822	4	US-09-248-796A-5145	Sequence 5145, Ap	C 186	13	81.2	1599	4	US-09-023-655-1485	Sequence 1405, Ap
C 114	14	87.5	3454	4	US-09-963-137-151	Sequence 137, App	C 187	13	81.2	1629	4	US-09-023-655-528	Sequence 528, App
C 115	14	87.5	3454	4	US-09-963-137-151	Sequence 137, App	C 188	13	81.2	1666	4	US-09-543-681A-951	Sequence 951, App
C 116	14	87.5	3728	1	US-08-111-939-1	Sequence 1, Appl	C 189	13	81.2	1873	4	US-09-370-767-12062	Sequence 12062, A
C 117	14	87.5	3935	3	US-09-060-482-1	Sequence 1, Appl	C 190	13	81.2	2088	4	US-09-448-796A-6792	Sequence 6792, Ap
C 118	14	87.5	4082	4	US-09-949-016-2122	Sequence 2122, Ap	C 191	13	81.2	2119	4	US-09-620-3120-35	Sequence 35, Appl
C 119	14	87.5	4265	4	US-09-540-236-1101	Sequence 1101, Ap	C 192	13	81.2	2151	4	US-09-540-236-193	Sequence 1913, Ap
C 120	14	87.5	6435	4	US-09-949-016-2884	Sequence 2884, Ap	C 193	13	81.2	2209	4	US-09-949-016-4507	Sequence 4507, App
C 121	14	87.5	6435	4	US-09-949-016-2885	Sequence 2885, Ap	C 194	13	81.2	2212	4	US-09-919-016-1277	Sequence 1277, A
C 122	14	87.5	6594	4	US-09-949-016-2990	Sequence 2990, Ap	C 195	13	81.2	2268	4	US-08-780-562-8	Sequence 8, Appl
C 123	14	87.5	6594	4	US-09-949-016-2991	Sequence 2991, Ap	C 196	13	81.2	3206	4	US-09-774-528-287	Sequence 287, App
C 124	14	87.5	13104	3	US-08-255-799-4	Sequence 4, Appl	C 197	13	81.2	3619	4	US-09-949-016-3496	Sequence 3496, Ap
C 125	14	87.5	13104	3	US-08-462-437-4	Sequence 4, Appl	C 198	13	81.2	4130	4	US-09-919-039-212	Sequence 212, App
C 126	14	87.5	14205	4	US-09-949-016-14464	Sequence 14464, A	C 199	13	81.2	4403	2	US-08-284-941-1	Sequence 1, Appl
C 127	14	87.5	21914	4	US-09-949-016-14626	Sequence 14626, A	C 200	13	81.2	4403	2	US-08-447-64-1	Sequence 1, Appl
C 128	14	87.5	21914	4	US-09-949-016-14627	Sequence 14627, A	C 201	13	81.2	4403	3	US-09-336-503-1	Sequence 1, Appl
C 129	14	87.5	21914	4	US-09-949-016-14732	Sequence 14732, A	C 202	13	81.2	4403	3	US-09-949-016-369	Sequence 1, Appl
C 130	14	87.5	21914	4	US-09-949-016-14733	Sequence 14733, A	C 203	13	81.2	4403	5	PCT-US93-02147A-1	Sequence 369, App
C 131	14	87.5	31063	4	US-09-596-002-20	Sequence 14733, A	C 204	13	81.2	5176	3	US-09-610-040-6	Sequence 1, Appl
C 132	14	87.5	37601	4	US-09-949-016-15516	Sequence 20, Appl	C 205	13	81.2	5176	3	US-10-267-761-6	Sequence 6, Appl
C 133	14	87.5	41613	4	US-09-949-016-15254	Sequence 15516, A	C 206	13	81.2	7210	4	US-09-634-238-15	Sequence 6, Appl
C 134	14	87.5	41613	4	US-09-949-016-15254	Sequence 15254, A	C 207	13	81.2	7236	3	US-09-949-016-15762	Sequence 15, Appl
C 135	14	87.5	107980	4	US-09-949-016-13765	Sequence 13765, A	C 208	13	81.2	10862	3	US-09-058-411-1	Sequence 15, Appl
C 136	14	87.5	128470	3	US-09-345-882-1	Sequence 13765, A	C 209	13	81.2	10862	4	US-09-705-949-1	Sequence 1, Appl
C 137	14	87.5	162450	3	US-09-949-016-15094	Sequence 15094, A	C 210	13	81.2	12566	3	US-09-452-638-52	Sequence 52, Appl
C 138	13	81.2	209210	1	US-08-281-106-50	Sequence 1, Appl	C 211	13	81.2	14705	4	US-08-961-527-149	Sequence 149, App
C 139	13	81.2	16	1	US-08-199-269-50	Sequence 50, Appl	C 212	13	81.2	14705	4	US-09-949-016-15249	Sequence 16449, A
C 140	13	81.2	16	1	US-08-758-626-14	Sequence 14, Appl	C 213	13	81.2	15995	4	US-09-949-016-15482	Sequence 15482, A
C 141	13	81.2	20	5	PCT-US94-07684-14	Sequence 14, Appl	C 214	13	81.2	24580	4	US-09-902-540-1227	Sequence 1227, Ap
C 142	13	81.2	21	1	US-08-281-106-49	Sequence 49, Appl	C 215	13	81.2	27490	4	US-08-311-731A-121	Sequence 121, App
C 143	13	81.2	21	1	US-08-199-269-49	Sequence 49, Appl	C 216	13	81.2	33110	1	US-08-306-691B-19	Sequence 19, Appl
C 144	13	81.2	25	4	US-09-336-196G-80393	Sequence 80393, A	C 217	13	81.2	35100	5	PCT-US93-06251-19	Sequence 19, Appl
C 145	13	81.2	25	4	US-09-336-196G-80393	Sequence 80393, A	C 218	13	81.2	35603	4	US-09-949-016-11863	Sequence 11863, A
C 146	13	81.2	25	4	US-09-336-196G-80394	Sequence 45, Appl	C 219	13	81.2	35604	4	US-09-949-016-12662	Sequence 12662, A
C 147	13	81.2	30	1	US-08-051-935A-45	Sequence 45, Appl	C 220	13	81.2	37715	4	US-09-949-016-13846	Sequence 13846, A
C 148	13	81.2	30	1	US-08-051-935A-46	Sequence 103, App	C 221	13	81.2	48149	4	US-09-949-016-15258	Sequence 15258, A
C 149	13	81.2	34	1	US-08-741-881-103	Sequence 103, App	C 222	13	81.2	51336	4	US-09-949-016-16054	Sequence 16054, A
C 150	13	81.2	34	1	US-08-739-158-103	Sequence 103, App	C 223	13	81.2	51336	4	US-09-949-016-12150	Sequence 12150, A
C 151	13	81.2	34	2	US-08-739-167-103	Sequence 103, App	C 224	13	81.2	52925	4	US-09-949-016-15374	Sequence 15374, A
C 152	13	81.2	34	3	US-08-404-796-103	Sequence 103, App	C 225	13	81.2	52925	4	US-09-949-016-11959	Sequence 11959, A
C 153	13	81.2	34	3	US-08-931-869-103	Sequence 103, App	C 226	13	81.2	65834	4	US-09-949-016-16336	Sequence 16336, A
C 154	13	81.2	34	3	US-08-483-511-8	Sequence 8, Appl	C 227	13	81.2	65834	4	US-09-949-016-12925	Sequence 12925, A
C 155	13	81.2	34	3	US-09-350-399-103	Sequence 103, App	C 228	13	81.2	79578	4	US-09-949-016-16336	Sequence 16336, A
C 156	13	81.2	34	3	US-09-336-140A-103	Sequence 103, App	C 229	13	81.2	84171	4	US-09-949-016-15374	Sequence 15374, A
C 157	13	81.2	35	1	PCT-US93-01009-8	Sequence 59, Appl	C 230	13	81.2	106929	4	US-09-949-016-12060	Sequence 12060, A
C 158	13	81.2	35	1	US-08-361-920-59	Sequence 59, Appl	C 231	13	81.2	106929	4	US-09-949-016-16518	Sequence 16518, A
C 159	13	81.2	35	1	US-08-479-939-59	Sequence 59, Appl	C 232	13	81.2	125188	4	US-09-949-016-11960	Sequence 11960, A
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C 161	13	81.2	223	4	US-09-134-000C-1948	Sequence 184, App	C 234	13	81.2	187848	4	US-09-949-016-12111	Sequence 12111, A
C 162	13	81.2	308	4	US-09-107-433-173	Sequence 173, App	C 235	13	81.2	250715	4	US-09-949-016-13294	Sequence 13294, A
C 163	13	81.2	308	4	US-09-107-433-173	Sequence 2036, Ap	C 236	13	81.2	251769	4	US-09-949-016-13185	Sequence 13185, A
C 164	13	81.2	348	4	US-09-502-540-2036	Sequence 27764, A	C 237	13	81.2	251769	4	US-09-949-016-13186	Sequence 13186, A
C 165	13	81.2	444	4	US-09-949-016-22874	Sequence 22874, A	C 238	13	81.2	266748	4	US-09-949-016-13187	Sequence 13187, A
C 166	13	81.2	541	4	US-09-949-016-22875	Sequence 22875, A	C 239	13	81.2	266748	4	US-09-949-016-13188	Sequence 13188, A
C 167	13	81.2	601	4	US-09-949-016-22876	Sequence 22876, A	C 240	13	81.2	266748	4	US-09-949-016-14577	Sequence 14577, A
C 168	13	81.2	601	4	US-09-949-016-22877	Sequence 22877, A	C 241	13	81.2	678533	4	US-09-949-016-14578	Sequence 14578, A
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C 171	13	81.2	601	4	US-09-949-016-153616	Sequence 153616, A	C 244	13	81.2	828152	2	US-08-501-968-36	Sequence 36, Appl
C 172	13	81.2	601	4	US-09-949-016-153616	Sequence 153616, A	C 245	13	75.0	16	5	PCT-US96-10984-36	Sequence 36, Appl
C 173	13	81.2	601	4	US-09-949-016-153616	Sequence 153616, A	C 246	13	75.0	16	5	PCT-US96-10984-36	Sequence 36, Appl

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C 248	12	75.0	17	4	US-09-940-244-184	Sequence 180, App	C 321	12	75.0	601	4	US-09-949-016-32261	Sequence 32261, A
C 249	12	75.0	19	4	US-09-940-244-180	Sequence 180, App	C 322	12	75.0	601	4	US-09-949-016-32483	Sequence 32483, A
C 250	12	75.0	20	4	US-09-940-244-187	Sequence 187, App	C 323	12	75.0	601	4	US-09-949-016-34472	Sequence 34472, A
C 251	12	75.0	20	4	US-09-940-244-188	Sequence 188, App	C 324	12	75.0	601	4	US-09-949-016-41367	Sequence 41367, A
C 252	12	75.0	20	4	US-09-940-244-189	Sequence 189, App	C 325	12	75.0	601	4	US-09-949-016-42434	Sequence 42434, A
C 253	12	75.0	21	4	US-09-940-244-174	Sequence 174, App	C 326	12	75.0	601	4	US-09-949-016-44303	Sequence 44303, A
C 254	12	75.0	21	4	US-09-940-244-181	Sequence 181, App	C 327	12	75.0	601	4	US-09-949-016-47080	Sequence 47080, A
C 255	12	75.0	21	4	US-09-940-244-186	Sequence 186, App	C 328	12	75.0	601	4	US-09-949-016-47081	Sequence 47081, A
C 256	12	75.0	22	4	US-09-940-244-182	Sequence 182, App	C 329	12	75.0	601	4	US-09-949-016-52711	Sequence 52711, A
C 257	12	75.0	25	4	US-09-396-196C-49597	Sequence 49597, A	C 330	12	75.0	601	4	US-09-949-016-56132	Sequence 56132, A
C 258	12	75.0	28	4	US-09-940-244-170	Sequence 170, App	C 331	12	75.0	601	4	US-09-949-016-56983	Sequence 56983, A
C 259	12	75.0	28	4	US-09-940-244-175	Sequence 175, App	C 332	12	75.0	601	4	US-09-949-016-57908	Sequence 57908, A
C 260	12	75.0	28	4	US-09-940-244-185	Sequence 185, App	C 333	12	75.0	601	4	US-09-949-016-60943	Sequence 60943, A
C 261	12	75.0	30	3	US-08-691-563C-69	Sequence 69, App	C 334	12	75.0	601	4	US-09-949-016-60944	Sequence 60944, A
C 262	12	75.0	30	4	US-09-374-766-69	Sequence 69, App	C 335	12	75.0	601	4	US-09-949-016-60947	Sequence 60947, A
C 263	12	75.0	30	4	US-08-979-847B-65	Sequence 65, App	C 336	12	75.0	601	4	US-09-949-016-63515	Sequence 63515, A
C 264	12	75.0	32	4	US-08-862-844-16	Sequence 16, App	C 337	12	75.0	601	4	US-09-949-016-63516	Sequence 63516, A
C 265	12	75.0	32	4	US-08-862-844-18	Sequence 18, App	C 338	12	75.0	601	4	US-09-949-016-63517	Sequence 63517, A
C 266	12	75.0	32	4	US-09-862-844-20	Sequence 20, App	C 339	12	75.0	601	4	US-09-949-016-67802	Sequence 67802, A
C 267	12	75.0	32	4	US-09-940-244-183	Sequence 183, App	C 340	12	75.0	601	4	US-09-949-016-84911	Sequence 84911, A
C 268	12	75.0	77	4	US-09-270-767-25832	Sequence 25832, A	C 341	12	75.0	601	4	US-09-949-016-84912	Sequence 84912, A
C 269	12	75.0	113	4	US-09-270-767-25142	Sequence 25142, A	C 342	12	75.0	601	4	US-09-949-016-84913	Sequence 84913, A
C 270	12	75.0	126	4	US-09-513-999C-22278	Sequence 22278, A	C 343	12	75.0	601	4	US-09-949-016-116771	Sequence 116771, A
C 271	12	75.0	175	4	US-09-621-976-16853	Sequence 16853, A	C 344	12	75.0	601	4	US-09-949-016-116772	Sequence 116772, A
C 272	12	75.0	177	1	US-08-392-678-20	Sequence 20, App	C 345	12	75.0	601	4	US-09-949-016-116772	Sequence 116772, A
C 273	12	75.0	177	1	US-08-457-304A-20	Sequence 20, App	C 346	12	75.0	601	4	US-09-949-016-118062	Sequence 118062, A
C 274	12	75.0	177	1	US-08-456-701A-20	Sequence 20, App	C 347	12	75.0	601	4	US-09-949-016-118063	Sequence 118063, A
C 275	12	75.0	177	3	US-08-684-532A-20	Sequence 20, App	C 348	12	75.0	601	4	US-09-949-016-137739	Sequence 137739, A
C 276	12	75.0	240	4	US-09-248-796A-8192	Sequence 8192, App	C 349	12	75.0	601	4	US-09-949-016-137748	Sequence 137748, A
C 277	12	75.0	243	4	US-09-540-236-1421	Sequence 1421, App	C 350	12	75.0	601	4	US-09-949-016-138165	Sequence 138165, A
C 278	12	75.0	265	4	US-09-270-767-28452	Sequence 28452, A	C 351	12	75.0	601	4	US-09-949-016-138166	Sequence 138166, A
C 279	12	75.0	287	4	US-09-313-294A-2940	Sequence 2940, App	C 352	12	75.0	601	4	US-09-949-016-148508	Sequence 148508, A
C 280	12	75.0	342	4	US-09-902-540-9053	Sequence 9053, App	C 353	12	75.0	601	4	US-09-949-016-150035	Sequence 150035, A
C 281	12	75.0	344	4	US-09-513-999C-10821	Sequence 10821, A	C 354	12	75.0	601	4	US-09-949-016-153918	Sequence 153918, A
C 282	12	75.0	379	4	US-09-621-976-11109	Sequence 11109, A	C 355	12	75.0	601	4	US-09-949-016-153998	Sequence 153998, A
C 283	12	75.0	386	4	US-09-270-767-2808	Sequence 2808, App	C 356	12	75.0	601	4	US-09-949-016-155999	Sequence 155999, A
C 284	12	75.0	386	4	US-09-270-767-18090	Sequence 18090, A	C 357	12	75.0	601	4	US-09-949-016-155999	Sequence 155999, A
C 285	12	75.0	386	4	US-09-640-173-59	Sequence 59, App	C 358	12	75.0	601	4	US-09-949-016-164830	Sequence 164830, A
C 286	12	75.0	386	4	US-09-713-550-59	Sequence 59, App	C 359	12	75.0	601	4	US-09-949-016-164830	Sequence 164830, A
C 287	12	75.0	396	4	US-08-825-294-59	Sequence 59, App	C 360	12	75.0	601	4	US-09-949-016-167052	Sequence 167052, A
C 288	12	75.0	396	4	US-09-970-966-59	Sequence 59, App	C 361	12	75.0	601	4	US-09-949-016-167053	Sequence 167053, A
C 289	12	75.0	396	4	US-09-270-767-31095	Sequence 31095, A	C 362	12	75.0	601	4	US-09-949-016-167053	Sequence 167053, A
C 290	12	75.0	412	4	US-09-602-787A-303	Sequence 303, App	C 363	12	75.0	601	4	US-09-949-016-170124	Sequence 170124, A
C 291	12	75.0	412	4	US-09-513-999C-3962	Sequence 3962, App	C 364	12	75.0	601	4	US-09-949-016-170380	Sequence 170380, A
C 292	12	75.0	421	4	US-09-270-767-9848	Sequence 9848, App	C 365	12	75.0	601	4	US-09-949-016-175187	Sequence 175187, A
C 293	12	75.0	426	4	US-09-513-999C-9924	Sequence 9924, App	C 366	12	75.0	601	4	US-09-949-016-175187	Sequence 175187, A
C 294	12	75.0	429	4	US-08-979-847B-135	Sequence 135, App	C 367	12	75.0	601	4	US-09-949-016-175198	Sequence 175198, A
C 295	12	75.0	429	4	US-08-979-847B-136	Sequence 136, App	C 368	12	75.0	601	4	US-09-949-016-175209	Sequence 175209, A
C 296	12	75.0	429	4	US-08-979-847B-137	Sequence 137, App	C 369	12	75.0	601	4	US-09-949-016-175456	Sequence 175456, A
C 297	12	75.0	429	4	US-08-979-847B-138	Sequence 138, App	C 370	12	75.0	601	4	US-09-949-016-177142	Sequence 177142, A
C 298	12	75.0	438	4	US-08-979-847B-128	Sequence 128, App	C 371	12	75.0	601	4	US-09-949-016-177659	Sequence 177659, A
C 299	12	75.0	438	4	US-08-979-847B-129	Sequence 129, App	C 372	12	75.0	601	4	US-09-949-016-187624	Sequence 187624, A
C 300	12	75.0	438	4	US-08-979-847B-130	Sequence 130, App	C 373	12	75.0	601	4	US-09-949-016-190556	Sequence 190556, A
C 301	12	75.0	438	4	US-08-979-847B-131	Sequence 131, App	C 374	12	75.0	601	4	US-09-949-016-192793	Sequence 192793, A
C 302	12	75.0	438	4	US-08-979-847B-201	Sequence 201, App	C 375	12	75.0	601	4	US-09-949-016-195071	Sequence 195071, A
C 303	12	75.0	441	4	US-09-248-796A-10012	Sequence 10012, A	C 376	12	75.0	601	4	US-09-949-016-199305	Sequence 199305, A
C 304	12	75.0	444	4	US-09-248-796A-1401	Sequence 1401, App	C 377	12	75.0	601	4	US-09-949-016-203890	Sequence 203890, A
C 305	12	75.0	453	4	US-09-909-595-13	Sequence 13, App	C 378	12	75.0	601	4	US-09-949-016-203394	Sequence 203394, A
C 306	12	75.0	466	4	US-09-270-767-10433	Sequence 10433, App	C 379	12	75.0	601	4	US-09-949-016-203395	Sequence 203395, A
C 307	12	75.0	500	4	US-09-270-767-5943	Sequence 5943, App	C 380	12	75.0	601	4	US-09-949-016-203396	Sequence 203396, A
C 308	12	75.0	500	4	US-09-270-767-20745	Sequence 20745, App	C 381	12	75.0	601	4	US-09-949-016-206272	Sequence 206272, A
C 309	12	75.0	516	3	US-09-173-151A-17	Sequence 17, App	C 382	12	75.0	601	4	US-09-949-016-206273	Sequence 206273, A
C 310	12	75.0	519	4	US-09-252-991A-1712	Sequence 1712, App	C 383	12	75.0	601	4	US-08-471-724-8	Sequence 8, App
C 311	12	75.0	525	4	US-09-270-767-14147	Sequence 14147, A	C 384	12	75.0	601	4	US-08-471-724-8	Sequence 8, App
C 312	12	75.0	528	4	US-09-270-767-12648	Sequence 12648, A	C 385	12	75.0	601	4	US-08-384-137-8	Sequence 8, App
C 313	12	75.0	532	4	US-09-621-976-19174	Sequence 19174, A	C 386	12	75.0	601	4	US-08-470-006A-8	Sequence 8, App
C 314	12	75.0	553	4	US-09-270-767-14843	Sequence 14843, A	C 387	12	75.0	601	4	US-08-691-563C-8	Sequence 8, App
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C 316	12	75.0	601	4	US-09-949-016-19000	Sequence 19000, A	C 389	12	75.0	601	4	US-09-133-411-8	Sequence 8, App
C 317	12	75.0	601	4	US-09-949-016-19001	Sequence 19001, A	C 390	12	75.0	601	4	US-09-374-766-8	Sequence 8, App
C 318	12	75.0	601	4	US-09-949-016-20068	Sequence 20068, A	C 391	12	75.0	601	4	US-08-979-847B-8	Sequence 8, App
C 319	12	75.0	601	4	US-09-949-016-20069	Sequence 20069, A	C 392	12	75.0	601	4	US-09-248-796A-707	Sequence 707, App

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417	12	75.0	921	4	US-09-252-991A-2100	Sequence 2100, Appl
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					US-08-979-847B-207	Sequence 207, Appl

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538	12	75.0	5636	4	US-09-949-016-14527	Sequence 14527, Appl

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573	12	75.0	8146	4	US-09-976-594-725	Sequence 725, App	646	12	75.0	45613	4	US-09-596-002-22	Sequence 22, Appl1
574	12	75.0	8298	5	PCT-US93-03076-1	Sequence 1, Appl1	647	12	75.0	45762	4	US-09-949-016-16651	Sequence 16651, A
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576	12	75.0	8523	4	US-09-172-422-2	Sequence 2, Appl1	649	12	75.0	46248	4	US-09-949-016-17327	Sequence 17327, A
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C 837	11	68.8	312	4	US-09-513-999C-879	Sequence 879, Ap	C 910	11	68.8	435	3	US-09-621-976-3558	Sequence 358, Ap
C 838	11	68.8	313	4	US-09-621-976-13417	Sequence 13417, A	C 911	11	68.8	435	4	US-09-270-767-8281	Sequence 2281, Ap
C 839	11	68.8	324	4	US-09-248-796A-8591	Sequence 8591, Ap	C 912	11	68.8	435	4	US-09-270-767-8285	Sequence 8285, Ap
C 840	11	68.8	326	3	US-09-564-805-212	Sequence 212, Ap	C 913	11	68.8	435	4	US-09-270-767-17563	Sequence 17563, A
C 841	11	68.8	329	4	US-09-621-976-71	Sequence 71, Appl	C 914	11	68.8	435	4	US-09-270-767-23567	Sequence 23567, A
C 842	11	68.8	332	4	US-09-513-999C-21292	Sequence 21292, A	C 915	11	68.8	435	4	US-09-621-976-1522	Sequence 1522, Ap
C 843	11	68.8	335	4	US-09-621-976-14610	Sequence 14610, A	C 916	11	68.8	435	4	US-09-513-999C-11313	Sequence 11313, A
C 844	11	68.8	342	4	US-09-489-039A-5145	Sequence 5145, Ap	C 917	11	68.8	435	4	US-09-621-976-126439	Sequence 12643, Ap
C 845	11	68.8	348	4	US-09-540-236-778	Sequence 778, Ap	C 918	11	68.8	435	4	US-09-621-976-3266	Sequence 3266, Ap
C 846	11	68.8	348	4	US-09-270-767-2398	Sequence 2398, Ap	C 919	11	68.8	435	4	US-09-949-016-89378	Sequence 89378, A
C 847	11	68.8	348	4	US-09-270-767-17680	Sequence 17680, A	C 920	11	68.8	435	4	US-09-621-976-1684	Sequence 1684, Ap
C 848	11	68.8	348	4	US-09-513-999C-338	Sequence 338, Ap	C 921	11	68.8	435	4	US-09-370-807-15	Sequence 15, Appl
C 849	11	68.8	349	4	US-09-270-767-65482	Sequence 26482, A	C 922	11	68.8	435	4	US-09-921-259-15	Sequence 15, Appl
C 850	11	68.8	352	4	US-09-621-976-17996	Sequence 17996, A	C 923	11	68.8	435	4	US-09-621-976-275	Sequence 275, Appl
C 851	11	68.8	353	4	US-09-621-976-16151	Sequence 16151, A	C 924	11	68.8	435	4	US-09-134-000C-6659	Sequence 21, Appl
C 852	11	68.8	359	3	US-09-404-879A-66	Sequence 66, Appl	C 925	11	68.8	435	4	US-09-312-283C-3352	Sequence 659, Appl
C 853	11	68.8	359	4	US-09-338-933-66	Sequence 66, Appl	C 926	11	68.8	435	4	US-09-385-982-473	Sequence 382, Ap
C 854	11	68.8	359	4	US-09-215-681-66	Sequence 66, Appl	C 927	11	68.8	435	4	US-09-385-982-473	Sequence 473, Ap
C 855	11	68.8	359	4	US-09-216-003A-66	Sequence 66, Appl	C 928	11	68.8	435	4	US-09-026-601-39	Sequence 39, Appl
C 856	11	68.8	359	4	US-09-667-857-66	Sequence 66, Appl	C 929	11	68.8	435	4	US-09-702-705-1753	Sequence 1753, Ap
C 857	11	68.8	363	4	US-09-513-999C-1733	Sequence 1733, Ap	C 930	11	68.8	435	4	US-09-736-457-1753	Sequence 1753, Ap
C 858	11	68.8	372	3	US-09-221-017B-317	Sequence 317, Ap	C 931	11	68.8	435	4	US-09-671-325-1753	Sequence 1753, Ap
C 859	11	68.8	375	4	US-09-107-433-1237	Sequence 1237, Ap	C 932	11	68.8	435	4	US-09-621-976-1526	Sequence 1526, Ap
C 860	11	68.8	382	4	US-09-270-767-706	Sequence 706, Ap	C 933	11	68.8	435	4	US-09-621-976-1526	Sequence 1526, Ap
C 861	11	68.8	382	4	US-09-270-767-15968	Sequence 15968, A	C 934	11	68.8	435	4	US-09-404-879A-56	Sequence 56, Appl
C 862	11	68.8	386	4	US-09-513-999C-927	Sequence 927, Ap	C 935	11	68.8	435	4	US-09-338-933-56	Sequence 56, Appl
C 863	11	68.8	390	4	US-09-513-999C-3075	Sequence 3075, Ap	C 936	11	68.8	435	4	US-09-215-681-56	Sequence 56, Appl
C 864	11	68.8	397	4	US-09-513-999C-225	Sequence 225, Ap	C 937	11	68.8	435	4	US-09-216-003A-56	Sequence 56, Appl
C 865	11	68.8	401	4	US-09-513-999C-3856	Sequence 3856, Ap	C 938	11	68.8	435	4	US-09-667-857-56	Sequence 56, Appl
C 866	11	68.8	408	4	US-09-465-529-77	Sequence 77, Appl	C 939	11	68.8	435	4	US-09-513-999C-10228	Sequence 10228, A
C 867	11	68.8	414	4	US-09-513-999C-1082	Sequence 1082, Ap	C 940	11	68.8	435	4	US-09-270-767-78	Sequence 78, Appl
C 868	11	68.8	419	3	US-09-328-111-478	Sequence 478, Ap	C 941	11	68.8	435	4	US-09-949-016-15360	Sequence 15360, A
C 869	11	68.8	423	4	US-09-702-705-573	Sequence 573, Ap	C 942	11	68.8	435	4	US-09-949-016-16233	Sequence 16233, A
C 870	11	68.8	423	4	US-09-736-457-573	Sequence 573, Ap	C 943	11	68.8	435	4	US-09-949-016-19310	Sequence 19310, A
C 871	11	68.8	423	4	US-09-614-124B-573	Sequence 573, Ap	C 944	11	68.8	435	4	US-09-949-016-19466	Sequence 19466, A
C 872	11	68.8	423	4	US-09-611-325-573	Sequence 573, Ap	C 945	11	68.8	435	4	US-09-949-016-21407	Sequence 21407, A
C 873	11	68.8	423	4	US-09-569-184-573	Sequence 573, Ap	C 946	11	68.8	435	4	US-09-949-016-21408	Sequence 21408, A
C 874	11	68.8	423	4	US-09-658-824-573	Sequence 573, Ap	C 947	11	68.8	435	4	US-09-949-016-21409	Sequence 21409, A
C 875	11	68.8	425	4	US-09-513-999C-3857	Sequence 3857, Ap	C 948	11	68.8	435	4	US-09-949-016-22380	Sequence 22380, A
C 876	11	68.8	429	4	US-09-513-999C-8354	Sequence 8354, Ap	C 949	11	68.8	435	4	US-09-949-016-24339	Sequence 24339, A
C 877	11	68.8	432	4	US-09-621-976-17808	Sequence 17808, A	C 950	11	68.8	435	4	US-09-949-016-24886	Sequence 24886, A
C 878	11	68.8	441	4	US-09-270-767-6479	Sequence 6479, Ap	C 951	11	68.8	435	4	US-09-949-016-25887	Sequence 25887, A
C 879	11	68.8	441	4	US-09-270-767-21761	Sequence 21761, A	C 952	11	68.8	435	4	US-09-949-016-26333	Sequence 26333, A
C 880	11	68.8	443	3	US-08-998-416-195	Sequence 195, Ap	C 953	11	68.8	435	4	US-09-949-016-26562	Sequence 26562, A
C 881	11	68.8	446	4	US-09-621-976-13235	Sequence 13235, A	C 954	11	68.8	435	4	US-09-949-016-26599	Sequence 26599, A
C 882	11	68.8	448	4	US-09-270-767-5665	Sequence 5665, Ap	C 955	11	68.8	435	4	US-09-949-016-27173	Sequence 27173, A
C 883	11	68.8	448	4	US-09-270-767-20947	Sequence 20947, A	C 956	11	68.8	435	4	US-09-949-016-27437	Sequence 27437, A
C 884	11	68.8	450	4	US-09-902-540-1640	Sequence 1640, Ap	C 957	11	68.8	435	4	US-09-949-016-27438	Sequence 27438, A
C 885	11	68.8	454	4	US-09-621-976-17461	Sequence 17461, A	C 958	11	68.8	435	4	US-09-949-016-28278	Sequence 28278, A
C 886	11	68.8	456	4	US-09-621-976-14151	Sequence 14151, A	C 959	11	68.8	435	4	US-09-949-016-28279	Sequence 28279, A
C 887	11	68.8	460	4	US-09-270-767-4284	Sequence 4284, Ap	C 960	11	68.8	435	4	US-09-949-016-28280	Sequence 28280, A
C 888	11	68.8	460	4	US-09-270-767-19566	Sequence 19566, A	C 961	11	68.8	435	4	US-09-949-016-28281	Sequence 28281, A
C 889	11	68.8	465	4	US-09-513-999C-32603	Sequence 32603, A	C 962	11	68.8	435	4	US-09-949-016-28282	Sequence 28282, A
C 890	11	68.8	470	3	US-09-328-111-439	Sequence 439, Ap	C 963	11	68.8	435	4	US-09-949-016-28283	Sequence 28283, A
C 891	11	68.8	471	4	US-09-248-796A-4073	Sequence 4073, Ap	C 964	11	68.8	435	4	US-09-949-016-29009	Sequence 29009, A
C 892	11	68.8	474	4	US-09-540-236-1158	Sequence 1158, Ap	C 965	11	68.8	435	4	US-09-949-016-29119	Sequence 29119, A
C 893	11	68.8	476	4	US-09-513-999C-13134	Sequence 13134, A	C 966	11	68.8	435	4	US-09-949-016-29640	Sequence 29640, A
C 894	11	68.8	477	4	US-09-513-999C-10326	Sequence 10326, A	C 967	11	68.8	435	4	US-09-949-016-29746	Sequence 29746, A
C 895	11	68.8	479	4	US-09-513-999C-8858	Sequence 8858, Ap	C 968	11	68.8	435	4	US-09-949-016-30278	Sequence 30278, A
C 896	11	68.8	479	4	US-09-471-276-770	Sequence 770, Ap	C 969	11	68.8	435	4	US-09-949-016-30292	Sequence 30292, A
C 897	11	68.8	482	4	US-09-621-976-16330	Sequence 16330, A	C 970	11	68.8	435	4	US-09-949-016-31675	Sequence 31675, A
C 898	11	68.8	482	4	US-09-513-999C-26168	Sequence 26168, A	C 971	11	68.8	435	4	US-09-949-016-33127	Sequence 33127, A
C 899	11	68.8	483	4	US-09-513-999C-32457	Sequence 32457, A	C 972	11	68.8	435	4	US-09-949-016-33323	Sequence 33323, A
C 900	11	68.8	485	4	US-09-621-976-2259	Sequence 2259, Ap	C 973	11	68.8	435	4	US-09-949-016-33324	Sequence 33324, A
C 901	11	68.8	485	4	US-08-600-430-3	Sequence 3, Appl1	C 974	11	68.8	435	4	US-09-949-016-33325	Sequence 33325, A
C 902	11	68.8	492	3	US-09-270-767-5537	Sequence 5537, Ap	C 975	11	68.8	435	4	US-09-949-016-33326	Sequence 33326, A
C 903	11	68.8	494	4	US-09-270-767-24819	Sequence 24819, A	C 976	11	68.8	435	4	US-09-949-016-33327	Sequence 33327, A

C 977 11 68.8 601 4 US-09-949-016-33328 Sequence 33328, A
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989 11 68.8 601 4 US-09-949-016-38500 Sequence 38500, A
990 11 68.8 601 4 US-09-949-016-39557 Sequence 39557, A
991 11 68.8 601 4 US-09-949-016-41564 Sequence 41564, A
992 11 68.8 601 4 US-09-949-016-43078 Sequence 43078, A
993 11 68.8 601 4 US-09-949-016-43207 Sequence 43207, A
994 11 68.8 601 4 US-09-949-016-43436 Sequence 43436, A
995 11 68.8 601 4 US-09-949-016-43665 Sequence 43665, A
996 11 68.8 601 4 US-09-949-016-44712 Sequence 44712, A
997 11 68.8 601 4 US-09-949-016-44713 Sequence 44713, A
998 11 68.8 601 4 US-09-949-016-44999 Sequence 44999, A
999 11 68.8 601 4 US-09-949-016-46329 Sequence 46329, A
C1000 11 68.8 601 4 US-09-949-016-46407 Sequence 46407, A

ALIGNMENTS

RESULT 1
US-08-281-106-48
Sequence 48, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Antisense Oligonucleotides Against
TITLE OF INVENTION: Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-48

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCACCACCAAGCA 16
Db 1 AAAGCACCACCAAGCA 16

RESULT 2
US-09-199-269-48
Sequence 48, Application US/09199269
Patent No. 6503533
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Antisense Oligonucleotides Against
TITLE OF INVENTION: Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-199-269-48

Query Match 100.0%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCACCACCAAGCA 16
Db 1 AAAGCACCACCAAGCA 16

RESULT 3
US-09-155-885A-41
Sequence 41, Application US/09155885A
Patent No. 6709812
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-155-885A-41
Query Match 100.0%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16
RESULT 4
US-08-480-220A-22
Sequence 22, Application US/08480220A
Patent No. 5667974
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla B.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770:US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' phosphate
LOCATION: 1
FEATURE:
NAME/KEY: 3' fluorescein
LOCATION: 18
US-08-480-220A-22
Query Match 100.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16
RESULT 5
US-08-864-404-22
Sequence 22, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3508
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla B.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770:US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' phosphate
LOCATION: 1
FEATURE:
NAME/KEY: 3' fluorescein
LOCATION: 18
US-08-864-404-22

Query Match 100.0%; Score 16; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCAAGCA 16
Db 1 AAAGCCACCAAGCA 16

RESULT 6
US-09-155-885A-49
Sequence 49, Application US/09155885A
Patent No. 6709812
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-155-885A-49

Query Match 100.0%; Score 16; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCAAGCA 16
Db 1 AAAGCCACCAAGCA 16

RESULT 7
US-08-480-220A-21/c
Sequence 21, Application US/08480220A
Patent No. 5667974
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/Abpd
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Potembek, Patricia E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-480-220A-21

Query Match 100.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCAAGCA 16
Db 18 AAAGCCACCAAGCA 3

RESULT 8
US-08-480-220A-25/c
Sequence 25, Application US/08480220A
Patent No. 5667974
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-480-220A-25

Query Match 100.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAGGCA 16
18 AAAGCCACCAGGCA 3
DB

RESULT 9
US-08-864-404-21/C
Sequence 21, Application US/08864404
Patent No. 595598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Iga K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-35008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-864-404-21

Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAGGCA 16
18 AAAGCCACCAGGCA 3
DB

RESULT 10
US-08-864-404-25/C
Sequence 25, Application US/08864404
Patent No. 595598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Iga K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-35008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA

FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-864-404-25

Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 18 AAAGCCACCCAGGCA 3

RESULT 11
US-08-501-968-18
Sequence 18, Application US/08501968
Patent No. 5985662
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowseart
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,968
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-501-968-18

Query Match 100.0%; Score 16; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 12
PCT-US96-10984-18
Sequence 18, Application PC/TUS9610984
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowseart
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
TITLE OF INVENTION: Virus Replication

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10984
FILING DATE: herewith
CLASSIFICATION:

PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-10984-18

Query Match 100.0%; Score 16; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 13
US-08-281-106-45
Sequence 45, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
TITLE OF INVENTION: Antisense Oligonucleotides Against
Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 66683/112/SEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-45

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 14
US-08-281-106-47
Sequence 47, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
NAME: GERIN, John L.
TITLE OF INVENTION: Antisense Oligonucleotides Against
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/SEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-47

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 6 AAAGCCACCCAGGCA 21

RESULT 15
US-08-287-337A-5
Sequence 5, Application US/08287337A
Patent No. 5728518
GENERAL INFORMATION:
APPLICANT: Ellen Carmichael
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,337A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConci, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-287-337A-5

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 6 AAAGCCACCCAGGCA 21

RESULT 16
US-08-501-968-7
Sequence 7, Application US/08501968
Patent No. 5985662
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowser
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,968
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-501-968-7

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 3 AAAGCCACCCAGGCA 18

RESULT 17
US-09-199-269-45
Sequence 45, Application US/09199269
Patent No. 6503533
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
GERIN, John L.
TITLE OF INVENTION: Antisense Oligonucleotides Against
Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-199-269-45

Query Match 100.0%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 18
US-09-199-269-47
Sequence 47, Application US/09199269
Patent No. 6503533
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
GERIN, John L.

TITLE OF INVENTION: Antisense Oligonucleotides Against
Hepatitis B Viral Replication

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-199-269-47

Query Match 100.0%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 6 AAAGCCACCCAGGCA 21

RESULT 19
PCT-US95-00508-5
Sequence 5, Application PC/TUS9500508

```

GENERAL INFORMATION:
APPLICANT: Targetech, Inc.
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00508
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/181,557
FILING DATE: January 12, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/287,337
FILING DATE: August 8, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-00508-5

Query Match          100.0%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAAGCCACCCAGGCA 16
Db      6 AAAGCCACCCAGGCA 21

```

```

RESULT 20
PCT-US96-10984-7
Sequence 7, Application PC/TUS9610984
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowbert
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

```

```

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10984
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-10984-7

Query Match          100.0%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAAGCCACCCAGGCA 16
Db      3 AAAGCCACCCAGGCA 18

```

```

RESULT 21
US-08-758-626-13/c
Sequence 13, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: Uwe Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,626
FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/422,018
FILING DATE:
APPLICATION NUMBER: 08/090,755
FILING DATE: JULY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainerd
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284, US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: nucleic acid

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-758-626-13

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 23 AAAGCCACCAAGCA 8

RESULT 22
PCT-US94-07684-13/c
Sequence 13, Application US/
GENERAL INFORMATION:

APPLICANT: ABBOTT LABORATORIES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,755
FILING DATE: JULY 13, 1993
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brinard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US94-07684-13

Query Match 100.0%; Score 16; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 23 AAAGCCACCAAGCA 8

RESULT 23
US-08-480-220A-19/c
Sequence 19, Application US/08480220A
Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushawat, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-480-220A-19

Query Match 100.0%; Score 16; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 18 AAAGCCACCAAGCA 3

RESULT 24
US-08-480-220A-20/c
Sequence 20, Application US/08480220A
Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushawat, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-480-220A-20

Query Match 100.0%; Score 16; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

RESULT 25
US-08-864-404-19/c
Sequence 19, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3508
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-864-404-19

Query Match 100.0%; Score 16; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

Db 18 AAAGCCACCCAGGCA 3

RESULT 26
US-08-864-404-20/c
Sequence 20, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3508
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-864-404-20

Query Match 100.0%; Score 16; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

RESULT 27
US-08-758-626-25/c
Sequence 25, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: Uwe Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA

```

;
; ZIP: 60064-3500
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,626
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,018
; FILING DATE:
; APPLICATION NUMBER: 08/090,755
; FILING DATE: JULY 13, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-937-4884
;
; INFORMATION FOR SEQ ID NO: 25:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
;
; US-08-758-626-25

Query Match          100.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCACCCCAAGCA 16
Db 23 AAAGCCACCCCAAGCA 8

RESULT 28
PCT-US94-07684-25/c
; Sequence 25, Application US/
; GENERAL INFORMATION:
; APPLICANT: ABBOTT LABORATORIES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
; TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,755
; FILING DATE: JULY 13, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
```

```

;
; LENGTH: 50
;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
;
; PCT-US94-07684-25

Query Match          100.0%; Score 16; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCACCCCAAGCA 16
Db 23 AAAGCCACCCCAAGCA 8

RESULT 29
US-08-890-735C-3/c
; Sequence 3, Application US/08890735C
; Patent No. 6518014
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HEPADNAVIRUS CORES
; FILE REFERENCE: DC44A
; CURRENT APPLICATION NUMBER: US/08/890,735C
; CURRENT FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 3
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
;
; US-08-890-735C-3

Query Match          100.0%; Score 16; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCACCCCAAGCA 16
Db 49 AAAGCCACCCCAAGCA 34

RESULT 30
US-08-098-313-10/c
; Sequence 10, Application US/08098313
; Patent No. 5532124
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University and
; APPLICANT: Timothy Block and Robert Graefstrom
; TITLE OF INVENTION: Genetically Engineered Bacteria To
; TITLE OF INVENTION: Identify and Produce Medically Important Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSER: Mackiewicz & No. 5532124r1s
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,313
; FILING DATE: October 6, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 654,064 and PCT/US91/07294
; FILING DATE: February 11, 1991 and October 4, 1991
```

ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardall
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-0638
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 69
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: no
US-08-098-313-10

Query Match 100.0%; Score 16; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 55 AAAGCCACCCAGGCA 40

RESULT 31
PCT-US92-01188-10/c
Sequence 10, Application PC/TUS9201188
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University and
APPLICANT: Timothy Block and Robert Grafstrom
TITLE OF INVENTION: Genetically Engineered Bacteria To
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESS: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01188
FILING DATE: 19910211
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 654,064 and PCT/US91/07294
FILING DATE: February 11, 1991 and October 4, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 69
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: no
PCT-US92-01188-10
Query Match 100.0%; Score 16; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 55 AAAGCCACCCAGGCA 40

RESULT 32
US-08-697-404-12/c
Sequence 12, Application US/08697404
Patent No. 5858732
GENERAL INFORMATION:
APPLICANT: N. A. Solomon
APPLICANT: S. R. Bouma
TITLE OF INVENTION: WIDE DYNAMIC RANGE NUCLEIC ACID
TITLE OF INVENTION: DETECTION USING AN AGGREGATE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,404
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,615A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yassier
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5692. US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-2341
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA (HBV)
US-08-697-404-12
Query Match 100.0%; Score 16; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 33 AAAGCCACCCAGGCA 18

RESULT 33
US-08-287-337A-9/c
Sequence 9, Application US/08287337A
Patent No. 5728518
GENERAL INFORMATION:
APPLICANT: Ellen Carmichael
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510

CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,337A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-287-337A-9

Query Match 100.0%; Score 16; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 49 AAAGCCACCCAGGCA 34

RESULT 34
US-08-075-520A-8/C
Sequence 8, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460

FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-8

Query Match 100.0%; Score 16; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10

RESULT 35
US-08-075-520A-11/C
Sequence 11, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-11

Query Match 100.0%; Score 16; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGCA 16
Db 25 AAAGCCACCCAGCA 10

RESULT 36

US-08-075-520A-16/c

; Sequence 16, Application US/08075520A
; Patent No. 6020167
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans
; TITLE OF INVENTION: A Composition Used as a
; TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas Popovich
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.520A
; FILING DATE: January 31, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124775
; FILING DATE: December 19, 1990
; APPLICATION NUMBER: PCT/EP91/02460
; FILING DATE: December 19, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-075-520A-16

Query Match 100.0%; Score 16; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGCA 16
Db 25 AAAGCCACCCAGCA 10

RESULT 37

US-08-445-585-2/c

; Sequence 2, Application US/08445585
; Patent No. 6277631
; GENERAL INFORMATION:
; APPLICANT: No. 6277631h, Michael
; APPLICANT: Broker, Michael
; TITLE OF INVENTION: Recombinant Proteins with the
; TITLE OF INVENTION: Immunoreactivity of Hepatitis B Virus B Antigen (HBsAg), A

; TITLE OF INVENTION: Process for the Preparation Thereof and the Use Thereof in
; TITLE OF INVENTION: Immunoassays and Vaccines
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,585
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 06-MAR-1992
; APPLICATION NUMBER: DE P 41 07 612.5
; FILING DATE: 03-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: P-36,228
; REFERENCE/DOCKET NUMBER: 02481.1162-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..477
; US-08-445-585-2

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 AAAGCCACCCAGCA 10

RESULT 38

US-08-075-520A-4/c

; Sequence 4, Application US/08075520A
; Patent No. 6020167
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans
; TITLE OF INVENTION: A Composition Used as a
; TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas Popovich
; ADDRESSEE: & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compag Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-4

Query Match 100.0%; Score 16; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 AAAGCCACCCCAAGCA 10

RESULT 39
US-08-075-520A-5/C
Sequence 5, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compag Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-5

Query Match 100.0%; Score 16; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 AAAGCCACCCCAAGCA 10

RESULT 40
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Sequence 35, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compag Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-35

Query Match 100.0%; Score 16; DB 3; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 AAAGCCACCCCAAGCA 10

Fri Apr 1 07:57:26 2005

us-09-888-164-29.oligo.rml

Page 23

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Job time : 120 secs

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	16	100.0	17	10	US-09-877-478-1755
5	16	100.0	17	17	US-10-342-902-1755
6	16	100.0	17	17	US-10-342-902-1755
7	16	100.0	17	18	US-10-669-841-1755
8	16	100.0	17	18	US-10-669-841-1755
9	16	100.0	17	18	US-10-453-792-49
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C 14	16	100.0	19	17	US-10-244-647-700	Sequence 700, App
C 15	16	100.0	19	17	US-10-244-647-1220	Sequence 1220, App
C 16	16	100.0	19	17	US-10-244-647-1222	Sequence 1222, App
C 17	16	100.0	19	17	US-10-244-647-1223	Sequence 1223, App
C 18	16	100.0	23	17	US-10-244-647-1296	Sequence 1296, App
C 19	16	100.0	54	9	US-09-756-500-4	Sequence 4, Appl
C 20	16	100.0	114	17	US-10-394-896-8	Sequence 8, Appl
C 21	16	100.0	291	17	US-10-394-896-11	Sequence 11, Appl
C 22	16	100.0	390	17	US-10-394-896-16	Sequence 16, Appl
C 23	16	100.0	534	17	US-10-394-896-4	Sequence 4, Appl
C 24	16	100.0	534	17	US-10-394-896-5	Sequence 5, Appl
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C 26	16	100.0	560	19	US-10-478-633A-70	Sequence 70, Appl
C 27	16	100.0	588	17	US-10-394-896-35	Sequence 35, Appl
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C 33	16	100.0	1841	17	US-10-398-221-3305	Sequence 3305, App
C 34	16	100.0	1977	17	US-10-461-790-97	Sequence 97, Appl
C 35	16	100.0	3161	17	US-10-453-792-301	Sequence 301, Appl
C 36	16	100.0	3182	9	US-09-929-955-14	Sequence 14, Appl
C 37	16	100.0	3182	13	US-10-104-966-14	Sequence 14, Appl
C 38	16	100.0	3182	17	US-10-453-792-302	Sequence 302, Appl
C 39	16	100.0	3182	17	US-10-453-792-303	Sequence 303, Appl
C 40	16	100.0	3182	17	US-10-453-792-304	Sequence 304, Appl
C 41	16	100.0	3182	17	US-10-453-792-305	Sequence 305, Appl
C 42	16	100.0	3182	17	US-10-453-792-306	Sequence 306, Appl
C 43	16	100.0	3182	17	US-10-453-792-307	Sequence 307, Appl
C 44	16	100.0	3182	17	US-10-453-792-308	Sequence 308, Appl
C 45	16	100.0	3182	17	US-10-719-619-14	Sequence 14, Appl
C 46	16	100.0	3182	18	US-10-817-591-14	Sequence 14, Appl
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C 52	16	100.0	3213	17	US-10-453-792-288	Sequence 288, Appl
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C 54	16	100.0	3214	17	US-10-453-792-290	Sequence 290, Appl
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C 80	16	100.0	4084	10	US-09-781-891D-22	Sequence 22, Appl
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C 82	16	100.0	5037	17	US-10-464-366-103	Sequence 103, Appl
C 83	16	100.0	5618	14	US-10-142-358-1	Sequence 1, Appl
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C 95	15	93.8	30	18	US-10-343-324-8	Sequence 8, Appl
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C 97	15	93.8	498	9	US-09-783-590-2423	Sequence 6984, Ap
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C 107	15	93.8	866	13	US-10-027-632-127158	Sequence 127158, A
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C 113	15	93.8	3215	17	US-10-453-792-296	Sequence 296, Ap
C 114	15	93.8	3215	17	US-10-453-792-297	Sequence 297, Ap
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C 169	14	87.5	609	13	US-10-425-115-72509	Sequence 72509, A
C 170	14	87.5	609	17	US-10-027-632-184552	Sequence 184552, A
C 171	14	87.5	610	13	US-10-027-632-184552	Sequence 184552, A
C 172	14	87.5	610	13	US-10-027-632-270155	Sequence 270155, A
C 173	14	87.5	633	13	US-10-027-632-18992	Sequence 18992, A
C 174	14	87.5	633	17	US-10-027-632-18992	Sequence 18992, A
C 175	14	87.5	761	17	US-10-312-045-30	Sequence 30, Appl
C 176	14	87.5	761	17	US-10-425-114-22100	Sequence 22100, A
C 177	14	87.5	831	17	US-10-424-599-138926	Sequence 138926, A
C 178	14	87.5	923	13	US-10-016-157A-83	Sequence 83, Appl
C 179	14	87.5	1006	17	US-10-177-55A-239	Sequence 239, Appl
C 180	14	87.5	1084	18	US-10-425-115-26435	Sequence 26435, A
C 181	14	87.5	1151	17	US-10-425-114-29152	Sequence 29152, A
C 182	14	87.5	1233	18	US-10-622-817-4	Sequence 4, Appl
C 183	14	87.5	1457	18	US-10-425-115-106219	Sequence 106219, A
C 184	14	87.5	1539	9	US-09-823-245A-591	Sequence 591, Appl
C 185	14	87.5	1533	17	US-10-388-93A-528	Sequence 528, Appl
C 186	14	87.5	1658	17	US-10-425-114-9034	Sequence 9034, Ap
C 187	14	87.5	1655	18	US-10-425-115-106221	Sequence 106221, A
C 188	14	87.5	1699	17	US-10-424-599-39276	Sequence 39276, A
C 189	14	87.5	2140	17	US-10-108-260A-513	Sequence 513, Appl
C 190	14	87.5	3454	9	US-09-963-137-151	Sequence 151, Appl
C 191	14	87.5	3454	9	US-09-963-137-178	Sequence 178, Appl
C 192	14	87.5	3454	9	US-09-962-929-1	Sequence 1, Appl
C 193	14	87.5	3454	10	US-09-963-131-151	Sequence 151, Appl
C 194	14	87.5	3454	10	US-09-963-131-178	Sequence 178, Appl
C 195	14	87.5	3454	11	US-09-997-722-194	Sequence 194, Appl
C 196	14	87.5	3454	17	US-10-703-864-48	Sequence 48, Appl
C 197	14	87.5	3523	17	US-10-264-049-490	Sequence 490, Appl
C 198	14	87.5	3522	14	US-10-116-802-133	Sequence 133, Appl
C 199	14	87.5	3535	14	US-10-238-876-1	Sequence 1, Appl
C 200	14	87.5	3535	15	US-10-177-293-88	Sequence 288, Appl
C 201	14	87.5	3535	17	US-10-159-553-288	Sequence 194, Appl
C 202	14	87.5	3535	18	US-10-775-920-195	Sequence 195, Appl
C 203	14	87.5	3535	18	US-10-473-974-128	Sequence 128, Appl
C 204	14	87.5	3535	18	US-10-473-974-128	Sequence 128, Appl
C 205	14	87.5	4125	18	US-10-775-920-198	Sequence 198, Appl
C 206	14	87.5	4236	17	US-10-282-122A-26916	Sequence 26916, A
C 207	14	87.5	6440	18	US-10-282-122A-26916	Sequence 26916, A
C 208	14	87.5	6599	18	US-10-719-993-367	Sequence 367, Appl
C 209	14	87.5	7697	10	US-09-952-213D-4	Sequence 267, Appl
C 210	14	87.5	1661	10	US-09-957-956-8	Sequence 4, Appl
C 211	14	87.5	29921	18	US-10-719-993-6848	Sequence 8, Appl
C 212	14	87.5	31063	17	US-10-719-993-6848	Sequence 6848, Ap
C 213	14	87.5	43229	13	US-10-087-192-517	Sequence 20, Appl
C 214	14	87.5	45855	17	US-10-087-192-517	Sequence 517, Appl
C 215	14	87.5	49226	11	US-09-997-722-193	Sequence 193, Appl
C 216	14	87.5	162450	15	US-10-071-179-1	Sequence 1, Appl
C 217	14	87.5	162450	16	US-10-126-704-1	Sequence 1, Appl
C 218	13	81.2	15	10	US-09-877-478-6017	Sequence 6017, Ap
C 219	13	81.2	15	17	US-10-342-902-6017	Sequence 6017, Ap
C 220	13	81.2	15	18	US-10-342-902-6017	Sequence 6017, Ap
C 221	13	81.2	15	18	US-10-669-841-2420	Sequence 2420, Ap
C 222	13	81.2	17	10	US-09-877-478-1150	Sequence 1150, Ap
C 223	13	81.2	17	10	US-09-877-478-1756	Sequence 1756, Ap
C 224	13	81.2	17	17	US-10-342-902-1150	Sequence 1150, Ap
C 225	13	81.2	17	18	US-10-342-902-1150	Sequence 1150, Ap
C 226	13	81.2	17	18	US-10-669-841-1150	Sequence 1150, Ap
C 227	13	81.2	19	17	US-10-669-841-1756	Sequence 1756, Ap
C 228	13	81.2	19	17	US-10-244-647-53	Sequence 53, Appl
C 229	13	81.2	21	17	US-10-244-647-599	Sequence 699, Appl
C 230	13	81.2	21	17	US-10-244-647-1371	Sequence 1371, Ap
C 230	13	81.2	21	17	US-10-244-647-1415	Sequence 1415, Ap

C 231	13	81.2	23	17	US-10-244-647-1305	Sequence 1305, Ap	304	13	81.2	587	18	US-10-021-323-12815	Sequence 12815, A
C 232	13	81.2	25	19	US-10-719-900-98205	Sequence 98205, A	305	13	81.2	592	18	US-10-021-323-8355	Sequence 8355, Ap
C 233	13	81.2	25	19	US-10-809-189-80393	Sequence 80393, A	306	13	81.2	598	17	US-10-027-632-230450	Sequence 230450, A
C 234	13	81.2	25	19	US-10-809-189-80394	Sequence 80394, A	307	13	81.2	598	17	US-10-027-632-230450	Sequence 230450, A
C 235	13	81.2	34	9	US-09-912-679-8	Sequence 8, Appl1	308	13	81.2	600	13	US-10-027-632-274642	Sequence 274642, A
C 236	13	81.2	34	9	US-09-466-035-8	Sequence 8, Appl1	309	13	81.2	600	13	US-10-027-632-274642	Sequence 274642, A
C 237	13	81.2	34	11	US-09-821-662-11	Sequence 11, Appl1	310	13	81.2	600	17	US-10-027-632-274642	Sequence 274642, A
C 238	13	81.2	34	17	US-10-346-880-103	Sequence 103, Appl	311	13	81.2	604	13	US-10-027-632-274643	Sequence 274643, A
C 239	13	81.2	34	17	US-10-150-407-103	Sequence 103, Appl	312	13	81.2	604	13	US-10-027-632-61763	Sequence 61763, A
C 240	13	81.2	34	17	US-10-384-245-965	Sequence 965, Appl	313	13	81.2	604	13	US-10-027-632-61764	Sequence 61764, A
C 241	13	81.2	141	18	US-10-425-115-99987	Sequence 99987, A	314	13	81.2	604	13	US-10-027-632-309949	Sequence 309949, A
C 242	13	81.2	163	17	US-10-424-599-34732	Sequence 34732, A	315	13	81.2	604	13	US-10-027-632-309950	Sequence 309950, A
C 243	13	81.2	173	18	US-10-425-115-91276	Sequence 91276, A	316	13	81.2	604	17	US-10-027-632-61763	Sequence 61763, A
C 244	13	81.2	193	17	US-10-424-599-12718	Sequence 12718, A	317	13	81.2	604	17	US-10-027-632-61764	Sequence 61764, A
C 245	13	81.2	201	19	US-10-741-600-56418	Sequence 56418, A	318	13	81.2	604	17	US-10-027-632-309949	Sequence 309949, A
C 246	13	81.2	207	9	US-09-738-626-2722	Sequence 2722, Ap	319	13	81.2	604	17	US-10-027-632-309950	Sequence 309950, A
C 247	13	81.2	223	17	US-10-424-599-53494	Sequence 53494, A	320	13	81.2	608	18	US-10-021-323-12795	Sequence 12795, A
C 248	13	81.2	228	16	US-10-029-386-27160	Sequence 27160, A	321	13	81.2	610	13	US-10-027-632-284833	Sequence 284833, A
C 249	13	81.2	231	18	US-10-723-860-4684	Sequence 4684, Ap	322	13	81.2	610	17	US-10-027-632-284833	Sequence 284833, A
C 250	13	81.2	240	9	US-09-864-761-21097	Sequence 21097, A	323	13	81.2	618	17	US-10-027-632-238664	Sequence 238664, A
C 251	13	81.2	286	18	US-10-425-115-5630	Sequence 5630, Ap	324	13	81.2	618	17	US-10-027-632-238664	Sequence 238664, A
C 252	13	81.2	289	17	US-10-702-075-261	Sequence 261, App	325	13	81.2	626	13	US-10-027-632-306191	Sequence 306191, A
C 253	13	81.2	291	17	US-10-424-599-95428	Sequence 95428, A	326	13	81.2	626	13	US-10-027-632-306191	Sequence 306191, A
C 254	13	81.2	308	17	US-10-424-599-107810	Sequence 107810, A	327	13	81.2	627	13	US-10-027-632-287327	Sequence 287327, A
C 255	13	81.2	339	18	US-10-723-860-884	Sequence 884, App	328	13	81.2	627	17	US-10-027-632-287327	Sequence 287327, A
C 256	13	81.2	343	9	US-09-960-352-7887	Sequence 7887, App	329	13	81.2	634	17	US-10-027-632-218555	Sequence 218555, A
C 257	13	81.2	365	17	US-10-113-664A-114	Sequence 114, App	330	13	81.2	634	17	US-10-027-632-218555	Sequence 218555, A
C 258	13	81.2	370	17	US-10-424-599-127598	Sequence 127598, A	331	13	81.2	640	13	US-10-027-632-125685	Sequence 125685, A
C 259	13	81.2	378	18	US-10-425-115-100567	Sequence 100567, A	332	13	81.2	640	13	US-10-027-632-125686	Sequence 125686, A
C 260	13	81.2	394	18	US-09-918-995-12878	Sequence 12878, A	333	13	81.2	640	13	US-10-027-632-125687	Sequence 125687, A
C 261	13	81.2	416	18	US-10-357-930-62003	Sequence 62003, A	334	13	81.2	640	17	US-10-027-632-125685	Sequence 125685, A
C 262	13	81.2	416	18	US-10-357-930-62038	Sequence 62038, A	335	13	81.2	640	17	US-10-027-632-125686	Sequence 125686, A
C 263	13	81.2	416	18	US-10-357-930-62136	Sequence 62136, A	336	13	81.2	640	17	US-10-027-632-125687	Sequence 125687, A
C 264	13	81.2	416	18	US-10-357-930-62195	Sequence 62195, A	337	13	81.2	642	17	US-10-282-1228-27561	Sequence 27561, A
C 265	13	81.2	420	9	US-09-933-797-450	Sequence 450, App	338	13	81.2	651	13	US-10-027-632-231754	Sequence 231754, A
C 266	13	81.2	423	13	US-10-027-632-88180	Sequence 88180, A	339	13	81.2	651	17	US-10-027-632-231754	Sequence 231754, A
C 267	13	81.2	423	17	US-10-027-632-88180	Sequence 88180, A	340	13	81.2	651	17	US-08-961-527-358	Sequence 358, App
C 268	13	81.2	427	9	US-09-867-701-5611	Sequence 5611, App	341	13	81.2	653	17	US-10-158-884-358	Sequence 358, App
C 269	13	81.2	446	18	US-10-425-115-51256	Sequence 51256, A	342	13	81.2	654	18	US-10-437-963-6623	Sequence 6623, Ap
C 270	13	81.2	446	18	US-10-767-701-16816	Sequence 16816, A	343	13	81.2	663	13	US-10-027-632-180652	Sequence 180652, A
C 271	13	81.2	449	9	US-09-864-761-4346	Sequence 4346, Ap	344	13	81.2	663	17	US-10-027-632-180652	Sequence 180652, A
C 272	13	81.2	453	18	US-10-437-963-8900	Sequence 8900, Ap	345	13	81.2	666	18	US-10-425-115-168808	Sequence 168808, A
C 273	13	81.2	454	10	US-09-918-995-22649	Sequence 22649, A	346	13	81.2	668	13	US-10-027-632-224984	Sequence 224984, A
C 274	13	81.2	464	9	US-09-864-761-1827	Sequence 1827, Ap	347	13	81.2	668	17	US-10-027-632-224984	Sequence 224984, A
C 275	13	81.2	465	13	US-10-027-632-268692	Sequence 268692, A	348	13	81.2	670	18	US-10-425-115-172633	Sequence 172633, A
C 276	13	81.2	465	17	US-10-027-632-268692	Sequence 268692, A	349	13	81.2	679	18	US-10-425-115-119888	Sequence 119888, A
C 277	13	81.2	469	18	US-10-425-115-109565	Sequence 109565, A	350	13	81.2	681	19	US-10-472-928-4127	Sequence 4127, Ap
C 278	13	81.2	469	18	US-10-357-930-58384	Sequence 58384, A	351	13	81.2	689	13	US-10-027-632-237921	Sequence 237921, A
C 279	13	81.2	474	10	US-09-918-995-28933	Sequence 28933, A	352	13	81.2	689	17	US-10-027-632-237921	Sequence 237921, A
C 280	13	81.2	478	10	US-09-918-995-1071	Sequence 1071, Ap	353	13	81.2	695	17	US-10-425-114-7387	Sequence 7387, Ap
C 281	13	81.2	487	18	US-10-021-323-6677	Sequence 6677, Ap	354	13	81.2	695	18	US-10-425-115-168803	Sequence 168803, A
C 282	13	81.2	488	17	US-10-424-599-76803	Sequence 76803, A	355	13	81.2	720	17	US-10-425-114-6357	Sequence 6357, Ap
C 283	13	81.2	489	18	US-10-437-963-56023	Sequence 56023, A	356	13	81.2	725	15	US-10-106-698-1657	Sequence 1657, Ap
C 284	13	81.2	490	17	US-10-424-599-55668	Sequence 55668, A	357	13	81.2	727	18	US-10-425-115-94463	Sequence 94463, A
C 285	13	81.2	498	10	US-09-918-995-11304	Sequence 11304, A	358	13	81.2	729	17	US-10-260-238-4417	Sequence 4417, Ap
C 286	13	81.2	503	10	US-09-918-995-28634	Sequence 28634, A	359	13	81.2	734	17	US-10-424-599-67163	Sequence 67163, A
C 287	13	81.2	516	19	US-10-696-639-2342	Sequence 2342, Ap	360	13	81.2	735	17	US-10-260-238-4418	Sequence 4418, Ap
C 288	13	81.2	519	13	US-10-027-632-275658	Sequence 275658, A	361	13	81.2	748	18	US-10-425-115-168805	Sequence 168805, A
C 289	13	81.2	519	17	US-10-027-632-275658	Sequence 275658, A	362	13	81.2	757	13	US-10-027-632-7332	Sequence 7332, Ap
C 290	13	81.2	519	18	US-10-021-323-12885	Sequence 12885, A	363	13	81.2	757	13	US-10-027-632-7332	Sequence 7332, Ap
C 291	13	81.2	526	18	US-10-021-323-12904	Sequence 12904, A	364	13	81.2	757	17	US-10-027-632-7332	Sequence 7332, Ap
C 292	13	81.2	530	18	US-10-425-115-109635	Sequence 109635, A	365	13	81.2	760	17	US-10-027-632-300355	Sequence 300355, A
C 293	13	81.2	530	18	US-10-425-115-151287	Sequence 151287, A	366	13	81.2	760	17	US-10-027-632-300356	Sequence 300356, A
C 294	13	81.2	533	13	US-10-027-632-193240	Sequence 193240, A	367	13	81.2	760	13	US-10-027-632-77187	Sequence 77187, A
C 295	13	81.2	533	17	US-10-027-632-193240	Sequence 193240, A	368	13	81.2	760	13	US-10-027-632-300356	Sequence 300356, A
C 296	13	81.2	537	16	US-10-029-386-13460	Sequence 13460, A	369	13	81.2	760	13	US-10-027-632-300357	Sequence 300357, A
C 297	13	81.2	539	18	US-10-653-047-2016	Sequence 2016, Ap	370	13	81.2	760	17	US-10-027-632-77187	Sequence 77187, A
C 298	13	81.2	555	13	US-10-027-632-43328	Sequence 43328, A	371	13	81.2	760	17	US-10-027-632-300355	Sequence 300355, A
C 299	13	81.2	555	13	US-10-027-632-43328	Sequence 43328, A	372	13	81.2	760	17	US-10-027-632-300356	Sequence 300356, A
C 300	13	81.2	555	17	US-10-027-632-43328	Sequence 43328, A	373	13	81.2	760	17	US-10-027-632-300357	Sequence 300357, A
C 301	13	81.2	555	17	US-10-027-632-43329	Sequence 43329, A	374	13	81.2	765	17	US-10-425-114-18617	Sequence 18617, A
C 302	13	81.2	565	18	US-10-021-323-3239	Sequence 3239, Ap	375	13	81.2	767	18	US-10-425-115-119920	Sequence 119920, A
C 303	13	81.2	567	18	US-10-021-323-13937	Sequence 13937, A	376	13	81.2	766	13	US-10-027-632-158263	Sequence 158263, A

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379	13	81.2	810	13	US-10-027-632-131375	Sequence 131375,	452	13	81.2	1726	18	US-10-723-860-5470	Sequence 5470, Ap
380	13	81.2	810	17	US-10-027-632-131374	Sequence 131374,	453	13	81.2	1741	9	US-09-823-45A-350	Sequence 350, App
381	13	81.2	810	17	US-10-027-632-131375	Sequence 131375,	454	13	81.2	1759	13	US-10-027-632-97509	Sequence 97509, A
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385	13	81.2	825	13	US-10-027-632-127198	Sequence 127198,	458	13	81.2	1781	13	US-10-027-632-100180	Sequence 100180, A
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396	13	81.2	900	13	US-10-424-599-67165	Sequence 67165, A	469	13	81.2	1884	17	US-10-027-632-99219	Sequence 99219, A
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404	13	81.2	933	17	US-10-374-780A-1380	Sequence 607, App	477	13	81.2	1884	17	US-10-027-632-99219	Sequence 99219, A
405	13	81.2	933	17	US-10-425-114-6246	Sequence 1380, Ap	478	13	81.2	2119	15	US-10-037-270-35	Sequence 34609, A
406	13	81.2	939	13	US-09-738-626-2678	Sequence 6246, Ap	479	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
407	13	81.2	939	13	US-10-027-632-381	Sequence 2678, Ap	480	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
408	13	81.2	939	13	US-10-027-632-381	Sequence 381, App	481	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
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411	13	81.2	983	14	US-10-116-275-287	Sequence 287, App	484	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
412	13	81.2	983	14	US-10-198-846-7285	Sequence 7285, Ap	485	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
413	13	81.2	996	9	US-10-424-599-74656	Sequence 74656, A	486	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
414	13	81.2	996	19	US-09-969-347-188	Sequence 188, App	487	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
415	13	81.2	1003	17	US-10-643-641A-8317	Sequence 8317, Ap	488	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
416	13	81.2	1083	17	US-10-369-493-36884	Sequence 36884, A	489	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
417	13	81.2	1095	9	US-09-925-298-183	Sequence 3, Appl	490	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
418	13	81.2	1095	14	US-10-102-806-183	Sequence 183, App	491	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
419	13	81.2	1110	17	US-10-369-493-26338	Sequence 26338, A	492	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
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422	13	81.2	1170	17	US-10-282-122A-11996	Sequence 11996, A	495	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
423	13	81.2	1188	18	US-10-767-701-9171	Sequence 9171, Ap	496	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
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425	13	81.2	1228	18	US-10-739-930-5138	Sequence 5138, Ap	498	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
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431	13	81.2	1327	17	US-10-424-599-67166	Sequence 67166, A	504	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
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434	13	81.2	1344	11	US-09-938-842A-5140	Sequence 5140, Ap	507	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
435	13	81.2	1381	17	US-10-172-116-1124	Sequence 1124, Ap	508	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
436	13	81.2	1381	17	US-10-342-887-1124	Sequence 1124, Ap	509	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
437	13	81.2	1381	18	US-10-335-053-250	Sequence 250, App	510	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
438	13	81.2	1404	17	US-10-369-493-27052	Sequence 27052, A	511	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
439	13	81.2	1469	17	US-10-424-599-71810	Sequence 71810, A	512	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
440	13	81.2	1469	17	US-10-424-599-81461	Sequence 81461, A	513	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
441	13	81.2	1471	17	US-10-374-780A-480	Sequence 480, App	514	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
442	13	81.2	1471	17	US-10-412-699B-981	Sequence 981, App	515	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
443	13	81.2	1480	18	US-10-437-963-57554	Sequence 57554, A	516	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
444	13	81.2	1518	17	US-10-369-493-42629	Sequence 42629, A	517	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
445	13	81.2	1525	9	US-09-880-107-3816	Sequence 3816, Ap	518	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
446	13	81.2	1536	18	US-10-425-115-168810	Sequence 168810, A	519	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
447	13	81.2	1562	18	US-10-437-963-36491	Sequence 36491, A	520	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
448	13	81.2	1589	17	US-10-641-643-1405	Sequence 1405, A	521	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A
449	13	81.2	1629	17	US-10-641-643-528	Sequence 528, App	522	13	81.2	2119	17	US-10-037-270-35	Sequence 34609, A

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C 525	13	81.2	4027	16	US-10-252-157-464	Sequence 464, App	C 598	12	75.0	13	10	US-09-877-478-6174	Sequence 6174, App
C 526	13	81.2	4130	10	US-09-919-039-212	Sequence 212, App	C 599	12	75.0	13	17	US-10-342-902-6174	Sequence 6174, App
527	13	81.2	4181	17	US-10-149-736-43	Sequence 43, Appl	C 600	12	75.0	13	18	US-10-669-841-2577	Sequence 2577, App
528	13	81.2	4181	19	US-10-364-536-43	Sequence 43, Appl	C 601	12	75.0	17	10	US-09-940-244-179	Sequence 179, App
529	13	81.2	4361	16	US-10-240-965-13	Sequence 13, Appl	C 602	12	75.0	17	10	US-09-940-244-184	Sequence 184, App
530	13	81.2	4403	9	US-09-880-107-2402	Sequence 2402, App	C 603	12	75.0	17	10	US-09-877-478-1149	Sequence 1149, App
531	13	81.2	4403	17	US-10-172-118-787	Sequence 787, App	C 604	12	75.0	17	10	US-09-864-638A-599	Sequence 599, App
532	13	81.2	4403	17	US-10-342-887-787	Sequence 787, App	C 605	12	75.0	17	10	US-09-864-638A-599	Sequence 599, App
533	13	81.2	4403	19	US-10-848-755A-105	Sequence 105, App	C 606	12	75.0	17	11	US-09-864-426A-599	Sequence 599, App
534	13	81.2	5106	18	US-10-437-963-101126	Sequence 101126, App	C 607	12	75.0	17	11	US-09-864-426A-599	Sequence 599, App
C 535	13	81.2	5176	14	US-10-267-763-6	Sequence 6, Appl1	C 608	12	75.0	17	16	US-10-084-833-613	Sequence 613, App
536	13	81.2	5394	18	US-10-437-963-101130	Sequence 101130, App	C 609	12	75.0	17	16	US-10-084-833-613	Sequence 613, App
537	13	81.2	5608	9	US-09-962-436-259	Sequence 259, App	C 610	12	75.0	17	17	US-10-342-902-61149	Sequence 1149, App
538	13	81.2	5608	9	US-09-880-107-1710	Sequence 1760, App	C 611	12	75.0	17	17	US-10-356-861-179	Sequence 179, App
539	13	81.2	5608	19	US-10-843-641A-2118	Sequence 2718, App	C 612	12	75.0	17	17	US-10-356-861-184	Sequence 184, App
540	13	81.2	5676	18	US-10-437-963-101128	Sequence 101128, App	C 613	12	75.0	17	18	US-10-669-841-1149	Sequence 1149, App
541	13	81.2	5937	18	US-10-437-963-101135	Sequence 101135, App	C 614	12	75.0	17	18	US-10-309-588-184	Sequence 184, App
542	13	81.2	6006	18	US-10-437-963-101132	Sequence 101132, App	C 615	12	75.0	17	18	US-10-309-588-184	Sequence 184, App
543	13	81.2	6835	9	US-09-070-927A-204	Sequence 204, App	C 616	12	75.0	18	16	US-10-290-386-184	Sequence 184, App
544	13	81.2	7210	17	US-10-264-213-15	Sequence 15, Appl	C 617	12	75.0	18	16	US-10-290-386-184	Sequence 184, App
C 545	13	81.2	8221	17	US-10-152-319A-2167	Sequence 2167, App	C 618	12	75.0	18	18	US-10-897-793-179	Sequence 179, App
546	13	81.2	9180	9	US-09-880-107-3461	Sequence 3461, App	C 619	12	75.0	18	18	US-10-897-793-184	Sequence 184, App
547	13	81.2	9180	18	US-10-723-860-4124	Sequence 4124, App	C 620	12	75.0	18	19	US-10-783-557-185	Sequence 185, App
C 548	13	81.2	10892	16	US-10-275-707-1	Sequence 1, Appl1	C 621	12	75.0	18	19	US-10-783-557-185	Sequence 185, App
C 549	13	81.2	10892	18	US-10-701-122-52	Sequence 52, App	C 622	12	75.0	19	10	US-09-940-244-180	Sequence 180, App
550	13	81.2	11839	10	US-09-764-891-7668	Sequence 7628, App	C 623	12	75.0	19	10	US-09-864-638A-614	Sequence 614, App
C 551	13	81.2	12566	8	US-08-961-527-149	Sequence 149, App	C 624	12	75.0	19	11	US-09-864-426A-614	Sequence 614, App
C 552	13	81.2	12566	17	US-10-158-844-149	Sequence 149, App	C 625	12	75.0	19	16	US-10-084-833-614	Sequence 614, App
553	13	81.2	15500	9	US-09-764-860-1091	Sequence 1091, App	C 626	12	75.0	19	17	US-10-244-647-56	Sequence 56, Appl
554	13	81.2	15500	14	US-10-074-095-1091	Sequence 1091, App	C 627	12	75.0	19	17	US-10-244-647-702	Sequence 702, App
555	13	81.2	15500	17	US-10-212-872-1091	Sequence 1091, App	C 628	12	75.0	19	17	US-10-356-861-180	Sequence 180, App
556	13	81.2	15576	17	US-10-292-798-639	Sequence 639, App	C 629	12	75.0	20	10	US-10-309-588-180	Sequence 180, App
557	13	81.2	19994	15	US-10-017-161-728	Sequence 729, App	C 630	12	75.0	20	10	US-09-940-244-188	Sequence 188, App
558	13	81.2	27204	13	US-10-087-192-158	Sequence 1528, App	C 631	12	75.0	20	10	US-09-940-244-188	Sequence 188, App
559	13	81.2	28486	16	US-10-004-113-25	Sequence 25, Appl	C 632	12	75.0	20	10	US-09-940-244-189	Sequence 189, App
560	13	81.2	28486	17	US-10-394-948-13	Sequence 13, Appl	C 633	12	75.0	20	10	US-09-864-638A-607	Sequence 607, App
561	13	81.2	30781	14	US-10-092-908-37	Sequence 37, Appl	C 634	12	75.0	20	10	US-09-864-638A-608	Sequence 608, App
562	13	81.2	34739	13	US-10-087-192-1846	Sequence 1846, App	C 635	12	75.0	20	10	US-09-864-638A-609	Sequence 609, App
C 563	13	81.2	37004	18	US-10-322-281-442	Sequence 442, App	C 636	12	75.0	20	11	US-09-864-426A-608	Sequence 608, App
564	13	81.2	37169	18	US-10-322-281-293	Sequence 293, App	C 637	12	75.0	20	11	US-09-864-426A-608	Sequence 608, App
C 565	13	81.2	42123	13	US-10-087-192-158	Sequence 1588, App	C 638	12	75.0	20	11	US-09-864-426A-609	Sequence 609, App
C 566	13	81.2	44051	17	US-10-085-117-4	Sequence 4, Appl1	C 639	12	75.0	20	16	US-10-290-386-180	Sequence 180, App
C 567	13	81.2	50295	11	US-09-997-722-259	Sequence 259, App	C 640	12	75.0	20	16	US-10-032-585-1587	Sequence 5187, App
568	13	81.2	52211	13	US-10-087-192-1567	Sequence 1567, App	C 641	12	75.0	20	16	US-10-084-833-607	Sequence 607, App
C 569	13	81.2	53714	17	US-10-052-482-142	Sequence 142, App	C 642	12	75.0	20	16	US-10-084-833-608	Sequence 608, App
C 570	13	81.2	57347	18	US-10-322-281-317	Sequence 317, App	C 643	12	75.0	20	16	US-10-084-833-609	Sequence 609, App
C 571	13	81.2	71864	13	US-10-087-192-1927	Sequence 1927, App	C 644	12	75.0	20	17	US-10-356-861-187	Sequence 187, App
C 572	13	81.2	72069	19	US-10-741-600-17775	Sequence 17775, A	C 645	12	75.0	20	17	US-10-356-861-188	Sequence 188, App
C 573	13	81.2	73771	13	US-10-087-192-1636	Sequence 1636, App	C 646	12	75.0	20	17	US-10-356-861-189	Sequence 189, App
C 574	13	81.2	75252	13	US-10-087-192-904	Sequence 904, App	C 647	12	75.0	20	18	US-10-309-588-187	Sequence 187, App
575	13	81.2	80423	18	US-10-367-094-41	Sequence 41, Appl	C 648	12	75.0	20	18	US-10-309-588-188	Sequence 188, App
C 576	13	81.2	87977	17	US-10-052-482-145	Sequence 145, App	C 649	12	75.0	20	18	US-10-309-588-189	Sequence 189, App
C 577	13	81.2	92638	18	US-10-450-826-3	Sequence 3, Appl1	C 650	12	75.0	20	18	US-10-897-793-180	Sequence 180, App
578	13	81.2	97952	18	US-10-741-601-5646	Sequence 5646, App	C 651	12	75.0	20	19	US-10-783-557-181	Sequence 181, App
579	13	81.2	107036	18	US-10-322-281-756	Sequence 756, App	C 652	12	75.0	21	10	US-09-940-244-174	Sequence 174, App
580	13	81.2	147708	18	US-10-450-826-61	Sequence 61, Appl	C 653	12	75.0	21	10	US-09-940-244-181	Sequence 181, App
C 581	13	81.2	177531	19	US-10-484-577-660	Sequence 660, App	C 654	12	75.0	21	10	US-09-940-244-186	Sequence 186, App
582	13	81.2	209484	13	US-10-087-192-418	Sequence 418, App	C 655	12	75.0	21	10	US-09-864-638A-600	Sequence 600, App
583	13	81.2	209484	18	US-10-331-053-4	Sequence 4, Appl1	C 656	12	75.0	21	10	US-09-864-638A-605	Sequence 605, App
C 584	13	81.2	223528	17	US-10-719-993-6856	Sequence 6856, App	C 657	12	75.0	21	11	US-09-864-638A-615	Sequence 615, App
C 585	13	81.2	269223	17	US-10-672-787-41	Sequence 41, Appl	C 658	12	75.0	21	11	US-09-864-426A-600	Sequence 600, App
C 586	13	81.2	289190	18	US-10-322-281-115	Sequence 115, App	C 659	12	75.0	21	11	US-09-864-426A-605	Sequence 605, App
C 587	13	81.2	313287	18	US-10-322-281-48	Sequence 48, Appl	C 660	12	75.0	21	11	US-09-864-426A-615	Sequence 615, App
C 588	13	81.2	337344	18	US-10-388-838-58	Sequence 58, Appl	C 661	12	75.0	21	16	US-10-290-386-186	Sequence 186, App
C 589	13	81.2	392112	18	US-10-812-232-3	Sequence 3, Appl1	C 662	12	75.0	21	16	US-10-290-386-187	Sequence 187, App
C 590	13	81.2	430442	18	US-10-417-375-128	Sequence 128, App	C 663	12	75.0	21	16	US-10-290-386-188	Sequence 188, App
C 591	13	81.2	653132	13	US-10-087-192-226	Sequence 226, App	C 664	12	75.0	21	16	US-10-290-386-189	Sequence 189, App
C 592	13	81.2	717651	18	US-10-719-993-6817	Sequence 6817, App	C 665	12	75.0	21	16	US-10-084-833-600	Sequence 600, App
593	13	81.2	2162598	19	US-10-472-928-4779	Sequence 4779, App	C 666	12	75.0	21	16	US-10-084-833-605	Sequence 605, App
594	13	81.2	2840917	13	US-10-027-633-114763	Sequence 114763, App	C 667	12	75.0	21	16	US-10-084-833-615	Sequence 615, App
595	13	81.2	2940917	17	US-10-027-633-114763	Sequence 114763, App	C 668	12	75.0	21	17	US-10-356-861-174	Sequence 174, App

C 669	12	75.0	21	17	US-10-356-861-181	Sequence 181, App	742	12	75.0	41	16	US-10-084-833-597	Sequence 597, App
C 670	12	75.0	21	17	US-10-356-861-186	Sequence 186, App	743	12	75.0	41	17	US-10-356-861-183	Sequence 183, App
C 671	12	75.0	21	18	US-10-309-584-174	Sequence 174, App	744	12	75.0	41	18	US-10-309-584-183	Sequence 183, App
C 672	12	75.0	21	18	US-10-309-584-181	Sequence 181, App	745	12	75.0	42	16	US-10-290-386-183	Sequence 183, App
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C 677	12	75.0	21	18	US-10-897-793-188	Sequence 188, App	750	12	75.0	65	19	US-10-908-975-367	Sequence 367, App
C 678	12	75.0	21	18	US-10-897-793-189	Sequence 189, App	751	12	75.0	65	10	US-09-908-975-4797	Sequence 4797, App
C 679	12	75.0	21	19	US-10-897-793-189	Sequence 189, App	752	12	75.0	119	17	US-10-424-599-14524	Sequence 14524, App
C 680	12	75.0	21	19	US-10-783-557-187	Sequence 187, App	753	12	75.0	150	18	US-10-767-701-15546	Sequence 15546, App
C 681	12	75.0	21	19	US-10-783-557-188	Sequence 188, App	754	12	75.0	160	17	US-10-242-538A-602	Sequence 602, App
C 682	12	75.0	21	19	US-10-783-557-189	Sequence 189, App	755	12	75.0	169	18	US-10-085-783A-602	Sequence 602, App
C 683	12	75.0	21	19	US-10-783-557-190	Sequence 190, App	756	12	75.0	169	18	US-10-437-963-32105	Sequence 32105, App
C 684	12	75.0	22	10	US-09-940-244-182	Sequence 182, App	757	12	75.0	183	18	US-10-425-115-164732	Sequence 164732, App
C 685	12	75.0	22	10	US-09-864-636A-616	Sequence 616, App	758	12	75.0	183	18	US-10-437-963-78559	Sequence 78559, App
C 686	12	75.0	22	11	US-09-864-636A-616	Sequence 616, App	759	12	75.0	183	18	US-10-437-963-78559	Sequence 78559, App
C 687	12	75.0	22	11	US-09-864-636A-616	Sequence 616, App	760	12	75.0	186	18	US-10-425-115-79951	Sequence 79951, App
C 688	12	75.0	22	16	US-10-290-386-174	Sequence 174, App	761	12	75.0	188	18	US-10-425-115-79951	Sequence 79951, App
C 689	12	75.0	22	16	US-10-290-386-181	Sequence 181, App	762	12	75.0	188	18	US-10-425-115-77051	Sequence 77051, App
C 690	12	75.0	22	16	US-10-084-833-616	Sequence 616, App	763	12	75.0	189	9	US-09-923-876-4768	Sequence 4768, App
C 691	12	75.0	22	18	US-10-356-861-182	Sequence 182, App	764	12	75.0	190	18	US-09-923-876-4768	Sequence 4768, App
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C 693	12	75.0	22	18	US-10-897-793-174	Sequence 174, App	766	12	75.0	190	18	US-10-425-115-78838	Sequence 78838, App
C 694	12	75.0	22	19	US-10-897-793-181	Sequence 181, App	767	12	75.0	201	18	US-10-741-601-14871	Sequence 14871, App
C 695	12	75.0	22	19	US-10-783-557-175	Sequence 175, App	768	12	75.0	201	18	US-10-741-601-14926	Sequence 14926, App
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C 697	12	75.0	23	16	US-10-290-386-182	Sequence 182, App	770	12	75.0	201	18	US-10-719-993-35740	Sequence 35740, App
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C 700	12	75.0	25	19	US-10-719-900-143951	Sequence 143951, App	773	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 701	12	75.0	25	19	US-10-719-900-83962	Sequence 83962, App	774	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 702	12	75.0	25	19	US-10-719-900-810679	Sequence 810679, App	775	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 703	12	75.0	25	19	US-10-809-189-49597	Sequence 49597, App	776	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 704	12	75.0	28	10	US-09-940-244-170	Sequence 170, App	777	12	75.0	207	18	US-10-425-115-153228	Sequence 153228, App
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C 706	12	75.0	28	10	US-09-940-244-185	Sequence 185, App	779	12	75.0	218	13	US-10-027-632-270309	Sequence 270309, App
C 707	12	75.0	28	10	US-09-864-636A-601	Sequence 601, App	780	12	75.0	219	9	US-10-027-632-270309	Sequence 270309, App
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C 709	12	75.0	28	11	US-09-864-636A-611	Sequence 611, App	782	12	75.0	223	18	US-10-437-963-79641	Sequence 79641, App
C 710	12	75.0	28	11	US-09-864-636A-611	Sequence 611, App	783	12	75.0	225	18	US-10-437-963-79641	Sequence 79641, App
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C 713	12	75.0	28	11	US-09-864-636A-611	Sequence 611, App	786	12	75.0	240	9	US-09-867-701-6277	Sequence 6277, App
C 714	12	75.0	28	16	US-10-084-833-601	Sequence 601, App	787	12	75.0	241	17	US-10-424-599-135621	Sequence 135621, App
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C 726	12	75.0	29	16	US-10-290-386-175	Sequence 170, App	799	12	75.0	266	18	US-10-425-115-58800	Sequence 58800, App
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C 825	12	75.0	323	17	US-10-424-599-36440	Sequence 36440, A	C 898	12	75.0	407	15	US-10-002-967A-431	Sequence 431, App
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964 12 75.0 419 13 US-10-027-632-56111 Sequence 56111, A
965 12 75.0 419 13 US-10-027-632-598919 Sequence 298919, A
966 12 75.0 419 17 US-10-027-632-56111 Sequence 56111, A
967 12 75.0 419 17 US-10-027-632-56111 Sequence 298919, A
968 12 75.0 419 18 US-10-027-632-298919 Sequence 298919, A
969 12 75.0 420 18 US-10-437-963-42332 Sequence 42332, A
C 970 12 75.0 420 18 US-10-367-094-78 Sequence 78, App1
C 971 12 75.0 423 11 US-08-732-627A-3376 Sequence 6148, App
972 12 75.0 423 18 US-10-425-115-135451 Sequence 3376, App
973 12 75.0 424 18 US-10-437-963-86247 Sequence 135451, A
974 12 75.0 428 8 US-10-424-599-110145 Sequence 86247, A
975 12 75.0 429 8 US-08-979-847-135 Sequence 110145, A
976 12 75.0 429 8 US-08-979-847-136 Sequence 135, App
977 12 75.0 429 8 US-08-979-847-137 Sequence 136, App
978 12 75.0 429 8 US-08-979-847-138 Sequence 137, App
979 12 75.0 429 8 US-08-979-847-138 Sequence 138, App
980 12 75.0 429 16 US-10-114-104-135 Sequence 135, App
981 12 75.0 429 16 US-10-114-104-136 Sequence 136, App
982 12 75.0 429 16 US-10-114-104-137 Sequence 137, App
983 12 75.0 429 18 US-10-114-104-138 Sequence 138, App
C 984 12 75.0 432 13 US-10-027-632-283398 Sequence 4628, App
C 985 12 75.0 432 13 US-10-027-632-283398 Sequence 283398, A
C 986 12 75.0 432 17 US-10-027-632-283398 Sequence 283398, A
C 987 12 75.0 432 17 US-10-027-632-283398 Sequence 283398, A
988 12 75.0 437 13 US-10-027-632-286410 Sequence 286410, A
989 12 75.0 437 17 US-10-027-632-286410 Sequence 286410, A
990 12 75.0 438 8 US-08-979-847-128 Sequence 128, App
991 12 75.0 438 8 US-08-979-847-129 Sequence 129, App
992 12 75.0 438 8 US-08-979-847-130 Sequence 130, App
993 12 75.0 438 8 US-08-979-847-131 Sequence 131, App
994 12 75.0 438 8 US-08-979-847-201 Sequence 201, App
995 12 75.0 438 10 US-09-918-995-2581 Sequence 2581, App
996 12 75.0 438 16 US-10-114-104-128 Sequence 128, App
997 12 75.0 438 16 US-10-114-104-129 Sequence 129, App
998 12 75.0 438 16 US-10-114-104-130 Sequence 130, App
999 12 75.0 438 16 US-10-114-104-131 Sequence 131, App
1000 12 75.0 438 16 US-10-114-104-201 Sequence 201, App

ALIGNMENTS

RESULT 1
US-09-888-164-29
Sequence 29, Application US/09888164
Publication No. US20030119724A1
GENERAL INFORMATION:
APPLICANT: T8'O, Paul O.P.
APPLICANT: Hangeland, Jon
APPLICANT: Deamond, Scott
APPLICANT: Roby, Clinton
TITLE OF INVENTION: LIGANDS TO ENHANCE CELLULAR UPTAKE OF BIOMOLECULES
FILE REFERENCE: 212241
CURRENT APPLICATION NUMBER: US/09/888, 164
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/282, 455
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 08/755, 062
PRIOR FILING DATE: 1996-11-22
PRIOR APPLICATION NUMBER: 60/007, 480
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Control oligomer
US-09-888-164-29

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGCCACCAAGGCA 16
Db 1 AAAGCCACCAAGGCA 16

RESULT 2
US-10-453-792-41
Sequence 41, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453, 792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155, 885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-453-792-41

Query Match 100.0%; Score 16; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCACCAAGGCA 16
Db 1 AAAGCCACCAAGGCA 16

RESULT 3
US-09-877-478-1755/c

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/ Sequence 1755, Application US/09877478
/ Publication No. US2003068301A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: Blact, Larry
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Morrissey, Dave
/ TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
/ FILE REFERENCE: MBH800-845-H (400/029)
/ CURRENT APPLICATION NUMBER: US/09/877,478
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: US 07/882,712
/ PRIOR FILING DATE: 1992-05-14
/ PRIOR APPLICATION NUMBER: US 09/531,025
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: US 09/636,385
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: US 09/696,347
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 08/193,627
/ PRIOR FILING DATE: 1994-02-07
/ PRIOR APPLICATION NUMBER: US 08/433,993
/ PRIOR FILING DATE: 1995-05-04
/ PRIOR APPLICATION NUMBER: US 08/434,504
/ PRIOR FILING DATE: 1995-05-04
/ PRIOR APPLICATION NUMBER: US 09/436,430
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 6586
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1755
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Hepatitis B virus
US-09-877-478-1755
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```
Query Match          100.0%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 1
```

```
RESULT 4
US-09-877-478-2378/c
/ Sequence 2378, Application US/09877478
/ Publication No. US2003068301A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: Blact, Larry
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Morrissey, Dave
/ TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
/ FILE REFERENCE: MBH800-845-H (400/029)
/ CURRENT APPLICATION NUMBER: US/09/877,478
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: US 07/882,712
/ PRIOR FILING DATE: 1992-05-14
/ PRIOR APPLICATION NUMBER: US 09/531,025
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: US 09/636,385
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: US 09/696,347
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 08/193,627
/ PRIOR FILING DATE: 1994-02-07
/ PRIOR APPLICATION NUMBER: US 08/433,993
/ PRIOR FILING DATE: 1995-05-04
/ PRIOR APPLICATION NUMBER: US 08/434,504
/ PRIOR FILING DATE: 1995-05-04
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/ PRIOR APPLICATION NUMBER: US 09/436,430
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 6586
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2378
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Hepatitis B virus
US-09-877-478-2378
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```
Query Match          100.0%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGCCACCCAGGCA 16
Db 17 AAAGCCACCCAGGCA 2
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```
RESULT 5
US-10-342-902-1755/c
/ Sequence 1755, Application US/10342902
/ Publication No. US20040054156A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: Blact, Larry
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Morrissey, Dave
/ TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
/ FILE REFERENCE: 400/075 (MBH800-845-1)
/ CURRENT APPLICATION NUMBER: US/10/342,902
/ CURRENT FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 09/877,478
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 09/531,025
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: US 09/636,385
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: US 09/696,347
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 08/193,627
/ PRIOR FILING DATE: 1994-02-07
/ PRIOR APPLICATION NUMBER: US 07/882,712
/ PRIOR FILING DATE: 1992-05-14
/ PRIOR APPLICATION NUMBER: US 09/436,430
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 6592
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1755
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Hepatitis B virus
US-10-342-902-1755
```

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Query Match          100.0%; Score 16; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 1
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```
RESULT 6
US-10-342-902-2378/c
/ Sequence 2378, Application US/10342902
/ Publication No. US20040054156A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: Blact, Larry
/ APPLICANT: McSwiggen, Jim
```

```
APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; PCT/US02/09187
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1993-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2378
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-2378

Query Match      100.0%; Score 16; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCAGGCA 16
Db      17 AAAGCCACCCAGGCA 2

RESULT 7
US-10-669-841-1755/c
; Sequence 1755, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
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; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-669-841-1755

Query Match      100.0%; Score 16; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCAGGCA 16
Db      16 AAAGCCACCCAGGCA 1

RESULT 8
US-10-669-841-2181/c
; Sequence 2181, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2181
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-669-841-2181

Query Match      100.0%; Score 16; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCAGGCA 16
```

Db 17 AAAGCCACCCAGGCA 2

RESULT 9
US-10-453-792-49

; Sequence 49, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI

; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998

APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996

ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2251-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-453-792-49

Query Match 100.0%; Score 16; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 1 AAAGCCACCCAGGCA 16

RESULT 10
US-10-244-647-54/C
; Sequence 54, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 54
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-54

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 19 AAAGCCACCCAGGCA 4

RESULT 11

US-10-244-647-574/C
; Sequence 574, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-574

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 17 AAAGCCACCCAGGCA 2

RESULT 12
US-10-244-647-576/c
; Sequence 576, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 576
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-576

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 1

RESULT 13
US-10-244-647-577/c
; Sequence 577, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-577

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 18 AAAGCCACCCAGGCA 3

RESULT 14
US-10-244-647-700
; Sequence 700, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-700

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 1 AAAGCCACCCAGGCA 16

RESULT 15
US-10-244-647-1220
; Sequence 1220, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1220
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1220

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 3 AAAGCCACCCAGGCA 18

RESULT 16
US-10-244-647-1222

Sequence 1222, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/10/244,647
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1222
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1222

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 4 AAAGCCACCCAGGCA 19

RESULT 17
US-10-244-647-1223

Sequence 1223, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647

CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1223
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1223

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 2 AAAGCCACCCAGGCA 17

RESULT 18
US-10-244-647-1296/c

Sequence 1296, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/10/244,647
PRIOR FILING DATE: 2003-04-14
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1296
LENGTH: 23
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-244-647-1296

Query Match 100.0%; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 23 AAAGCCACCCAGGCA 8

RESULT 19
US-09-756-500-4/c

Sequence 4, Application US/09756500
Patent No. US20010001098A1
GENERAL INFORMATION:
APPLICANT: Lu, Shan

APPLICANT: Huang, Zulu
TITLE OF INVENTION: HEPATITIS B CORE ANTIGEN NUCLEIC ACID
FILE REFERENCE: 07917-077002
CURRENT APPLICATION NUMBER: US/09/756,500
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 09/400,497
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 60/101,311
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 54
TYPE: RNA
ORGANISM: Human Hepatitis B Virus
US-09-756-500-4

Query Match 100.0%; Score 16; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCCAAGCA 16
Db 43 AAAGCCACCCCAAGCA 28

RESULT 20
US-10-394-896-8/c
Sequence 8, Application US/10394896
Publication No. US20030235591A1
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/394,896
FILING DATE: MARCH 21, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 114 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-10-394-896-8

Query Match 100.0%; Score 16; DB 17; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCCAAGCA 16
Db 25 AAAGCCACCCCAAGCA 10

RESULT 21
US-10-394-896-11/c
Sequence 11, Application US/10394896
Publication No. US20030235591A1
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/394,896
FILING DATE: MARCH 21, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-10-394-896-11

Query Match 100.0%; Score 16; DB 17; Length 291;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCCAAGCA 16
Db 25 AAAGCCACCCCAAGCA 10

RESULT 22

US-10-394-896-16/C

; Sequence 16, Application US/10394896
; Publication No. US20030235591A1

; GENERAL INFORMATION:

; APPLICANT: Thoma, Hans

; TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Thomas E. Popovich, Thomas Popovich

; ADDRESSEE: & Associates

; STREET: 80 South 8th Street

; CITY: Minneapolis

; STATE: Minnesota

; COUNTRY: USA

; ZIP: 55402-2111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

; MEDIUM TYPE: Storage

; COMPUTER: IBM Compatible Compaq Prolinea 4/66

; OPERATING SYSTEM: MS-DOS Version 5

; SOFTWARE: Microsoft Word for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/394,896

; FILING DATE: MARCH 21, 2003

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/075,520A

; FILING DATE: January 31, 1994

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (612) 334-8991

; TELEFAX: (612) 334-8994

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 bp

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-10-394-896-16

Query Match 100.0%; Score 16; DB 17; Length 390;
Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 16
DB 25 AAGCCACCCAGGCA 10

RESULT 23

US-10-394-896-4/C

; Sequence 4, Application US/10394896

; Publication No. US20030235591A1

; GENERAL INFORMATION:

; APPLICANT: Thoma, Hans

; TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Thomas E. Popovich, Thomas Popovich

ADDRESSEE: & Associates
STREET: 80 South 8th Street

CITY: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55402-2111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compaq Prolinea 4/66

OPERATING SYSTEM: MS-DOS Version 5

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/394,896

FILING DATE: MARCH 21, 2003

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/075,520A

FILING DATE: January 31, 1994

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 334-8991

TELEFAX: (612) 334-8994

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 534 bp

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-10-394-896-4

Query Match 100.0%; Score 16; DB 17; Length 534;
Best Local Similarity 100.0%; Pred. No. 6.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 16
DB 25 AAGCCACCCAGGCA 10

RESULT 24

US-10-394-896-5/C

; Sequence 5, Application US/10394896

; Publication No. US20030235591A1

; GENERAL INFORMATION:

; APPLICANT: Thoma, Hans

; TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Thomas E. Popovich, Thomas Popovich

; ADDRESSEE: & Associates

; STREET: 80 South 8th Street

; CITY: Minneapolis

; STATE: Minnesota

; COUNTRY: USA

; ZIP: 55402-2111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compaq Prolinea 4/66

OPERATING SYSTEM: MS-DOS Version 5

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

```
APPLICATION NUMBER: US/10/394,896
FILING DATE: MARCH 21, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-10-394-896-5
```

```
Query Match 100.0%; Score 16; DB 17; Length 534;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10
```

```
RESULT 25
US-10-478-633A-69/c
Sequence 69, Application US/10478633A
Publication No. US20050059000A1
GENERAL INFORMATION:
APPLICANT: TAKARA BIO INC.
TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
FILE REFERENCE: 663232
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: JP 2001-177737
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2001-249689
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 69
LENGTH: 560
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-478-633A-69
```

```
Query Match 100.0%; Score 16; DB 19; Length 560;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAAGCCACCCAGGCA 16
Db 529 AAAGCCACCCAGGCA 514
```

```
RESULT 26
US-10-478-633A-70/c
Sequence 70, Application US/10478633A
Publication No. US20050059000A1
GENERAL INFORMATION:
APPLICANT: TAKARA BIO INC.
```

```
TITLE OF INVENTION: A stabilization method and a preservation method for a reagent f
TITLE OF INVENTION: acid amplification or detection reaction
FILE REFERENCE: 663232
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: JP 2001-177737
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2001-249689
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 70
LENGTH: 560
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-478-633A-70
```

```
Query Match 100.0%; Score 16; DB 19; Length 560;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAAGCCACCCAGGCA 16
Db 529 AAAGCCACCCAGGCA 514
```

```
RESULT 27
US-10-394-896-35/c
```

```
Sequence 35, Application US/10394896
Publication No. US2003023591A1
GENERAL INFORMATION:
```

```
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
```

```
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
```

```
ADDRESS: & Associates
```

```
STREET: 80 South 8th Street
```

```
CITY: Minneapolis
```

```
STATE: Minnesota
```

```
COUNTRY: USA
```

```
ZIP: 55402-2111
```

```
COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
```

```
MEDIUM TYPE: Storage
```

```
COMPUTER: IBM Compatible Compaq Prolinea 4/66
```

```
OPERATING SYSTEM: MS-DOS Version 5
```

```
SOFTWARE: Microsoft Word for Windows
```

```
CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/10/394,896
```

```
FILING DATE: MARCH 21, 2003
```

```
CLASSIFICATION:
```

```
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US/08/075,520A
```

```
FILING DATE: January 31, 1994.
```

```
CLASSIFICATION:
```

```
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: EP 90124775
```

```
FILING DATE: December 19, 1990
```

```
APPLICATION NUMBER: PCT/EP91/02460
```

```
FILING DATE: December 19, 1991
```

```
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Thomas E. Popovich
```

```
REGISTRATION NUMBER: 30099
```

```
REFERENCE/DOCKET NUMBER: 3757/MED1001US
```

```
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (612) 334-8991
```

```
TELEFAX: (612) 334-8994
```

```
INFORMATION FOR SEQ ID NO: 35:
```

```
SEQUENCE CHARACTERISTICS:
```

```
LENGTH: 588 bp
```

```
TYPE: Nucleic Acid
```

```
STRANDEDNESS: Single
```

TOPOLOGY: Linear
US-10-394-896-35

Query Match 100.0%; Score 16; DB 17; Length 588;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 25 AAAGCCACCCAGGCA 10

RESULT 28
US-10-312-045-1/c
; Sequence 1, Application US/10312045
; Publication No. US20040054139A1
; GENERAL INFORMATION:
; APPLICANT: Mark PAGE
; APPLICANT: Jing-Li Li
; APPLICANT: Paul PUMPHENS
; APPLICANT: Galina BORISOVA
; TITLE OF INVENTION: MODIFICATION OF HEPATITIS B CORE ANTIGEN
; FILE REFERENCE: 117-432 / N78451B
; CURRENT APPLICATION NUMBER: US/10/312,045
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: PCT/GB01/02817
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: GB 0024544.9
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: GB 0015308.0
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(639)
US-10-312-045-1

Query Match 100.0%; Score 16; DB 17; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 82 AAAGCCACCCAGGCA 67

RESULT 29
US-10-240-917-1/c
; Sequence 1, Application US/10240917
; Publication No. US2004023965A1
; GENERAL INFORMATION:
; APPLICANT: Annick GELIN
; APPLICANT: Robert GILBERT
; APPLICANT: David STUART
; APPLICANT: David ROWLANDS
; TITLE OF INVENTION: HEPATITIS B CORE ANTIGEN FUSION PROTEINS
; FILE REFERENCE: 117-419 / N79405B
; CURRENT APPLICATION NUMBER: US/10/240,917
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/GB01/01607
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: EP 00107118.2
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: MS Word
; SEQ ID NO 1
; LENGTH: 639
; TYPE: DNA

ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(639)
US-10-240-917-1

Query Match 100.0%; Score 16; DB 18; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 82 AAAGCCACCCAGGCA 67

RESULT 30
US-09-912-679-56/c
; Sequence 56, Application US/09912679
; Patent No. US20020141974A1
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; Lee, William T.L.
; Townsend, Kay
; O'Dea, Joanne
; TITLE OF INVENTION: HEPATITIS THERAPEUTICS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/912,679
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.407C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-912-679-56

Query Match 100.0%; Score 16; DB 9; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 92 AAAGCCACCCAGGCA 77

RESULT 31
US-09-466-035-56/c
; Sequence 56, Application US/09466035
; Patent No. US20020165172A1

```

; GENERAL INFORMATION:
; APPLICANT: SALIBERG, MATTI
; LEE, WILLIAM T.I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; INTRACELLULAR DISEASES
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robins & Pasternak LLP
; STREET: 545 Middlefield Road, Suite 180
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,035
; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasternak, Daina S.
; REGISTRATION NUMBER: 41,411
; REFERENCE/DOCKET NUMBER: 2300-1231.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-325-7812
; TELEFAX: 650-325-7823
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-466-035-56

Query Match      100.0%; Score 16; DB 9; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
DB      92 AAAGCCACCCCAAGCA 77

RESULT 32
US-09-821-662-23/C
; Sequence 23, Application US/09821662
; Publication No. US20040063652A1
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; Montisano, Dominic
; TITLE OF INVENTION: COMBINATION GENE DELIVERY VEHICLE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/821,662
; FILING DATE: 29-Mar-2001
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; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 930049.428
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELE: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-821-662-23
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Query Match      100.0%; Score 16; DB 11; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 AAAGCCACCCCAAGCA 16
DB      92 AAAGCCACCCCAAGCA 77
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RESULT 33
US-10-398-221-3305
; Sequence 3305, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3305
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Listeria monocytogenes 4b
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3305
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Query Match      100.0%; Score 16; DB 17; Length 1841;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AAAGCCACCCCAAGCA 16
DB      105 AAAGCCACCCCAAGCA 120
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RESULT 34
US-10-461-790-97/C
; Sequence 97, Application US/10461790
; Publication No. US20040029111A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
```

APPLICANT: Dockter, Janel M.
APPLICANT: Getman, Damon K.
APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Loy, Marcy
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GP134-02.UT
CURRENT APPLICATION NUMBER: US/10/461,790
PRIORITY FILING DATE: 2003-06-13
PRIORITY FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 97
LENGTH: 1977
TYPE: DNA
ORGANISM: Hepatitis B Virus
US-10-461-790-97

Query Match 100.0%; Score 16; DB 17; Length 1977;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1883 AAAGCCACCCAGGCA 1868

RESULT 35
US-10-453-792-301/c

Sequence 301, Application US/10453792
Publication No. US20040029110A1

GENERAL INFORMATION:

APPLICANT: STUYVER, LIEVEN

ROSSAU, RUDI

MAERTENS, GEERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

NUMBER OF SEQUENCES: 313

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/453,792

FILING DATE: 04-Jun-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,885A

FILING DATE: 08-Oct-1998

APPLICATION NUMBER: PCT/EP97/02002

FILING DATE: 21-APR-1997

APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 301:

SEQUENCE CHARACTERISTICS:

LENGTH: 3161 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 301:
US-10-453-792-301

Query Match 100.0%; Score 16; DB 17; Length 3161;
Best Local Similarity 100.0%; Pred. No. 5.3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1876 AAAGCCACCCAGGCA 1861

RESULT 36
US-09-929-955-14/c

Sequence 14, Application US/09929955

Patent No. US20020136740A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg

APPLICANT: Catharina Hultgren

TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND

FILE REFERENCE: TRIPEP.23AUS2

CURRENT APPLICATION NUMBER: US/09/929,955

PRIORITY FILING DATE: 2001-08-15

PRIORITY FILING DATE: 09/705,547

PRIORITY FILING DATE: 2000-11-03

PRIORITY FILING DATE: 2000-11-03

PRIORITY FILING DATE: 2000-08-29

PRIORITY FILING DATE: 2000-08-29

PRIORITY FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 3182

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Hepatitis B virus sequence

US-09-929-955-14

Query Match 100.0%; Score 16; DB 9; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1897 AAAGCCACCCAGGCA 1882

RESULT 37
US-10-104-966-14/c

Sequence 14, Application US/10104966

Publication No. US20020155124A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg

APPLICANT: Catharina Hultgren

TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND

FILE REFERENCE: TRIPEP.23AUS2

CURRENT APPLICATION NUMBER: US/10/104,966

PRIORITY FILING DATE: 2002-03-22

PRIORITY FILING DATE: 2000-11-03

PRIORITY FILING DATE: 2000-11-03

PRIORITY FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 3182
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hepatitis B virus sequence
US-10-104-966-14

Query Match 100.0%; Score 16; DB 13; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
DB 1897 AAAGCACCACCAAGCA 1882

RESULT 38
US-10-453-792-302/c
Sequence 302, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 302:
US-10-453-792-302

Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCACCACCAAGCA 16

DB 1897 AAAGCACCACCAAGCA 1882

RESULT 39
US-10-453-792-303/c
Sequence 303, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 303:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 303:
US-10-453-792-303

Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
DB 1897 AAAGCACCACCAAGCA 1882

RESULT 40
US-10-453-792-304/c
Sequence 304, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 304:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 304:
US-10-453-792-304
Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0; Gaps 0;
Qy 1 AAAGCCACCCAGGCA 16
Db 1897 AAAGCCACCCAGGCA 1882

Search completed: March 31, 2005, 14:14:42
Job time : 298 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:05:43 ; Search time 1558 Seconds

(without alignments)
390.904 Million cell updates/sec

Title: US-09-888-164-29

Perfect score: 16

Sequence: 1 aaagcaccacgaagca 16

Scoring table: OLIGO_NUC

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	384	2	BP327943
2	16	100.0	396	4	BI049449
3	16	100.0	441	9	CE327035
4	16	100.0	464	1	AA103554
5	16	100.0	496	2	BI144757
6	16	100.0	587	7	CF755881
7	16	100.0	623	5	B0385327
8	16	100.0	646	6	CA192813
9	16	100.0	659	2	BB545848
10	16	100.0	666	6	CA083440
11	16	100.0	700	1	AV359761
12	16	100.0	770	6	CD778583
13	16	100.0	895	4	BI250824
14	16	100.0	975	6	CA474404
15	16	100.0	987	7	W34362
16	16	100.0	1684	9	CG754259
17	16	100.0	2005	3	AK009491
18	16	100.0	2368	3	AK078669
19	15	93.8	231	2	BI198017
20	15	93.8	268	2	BP924007
21	15	93.8	285	2	BB090939
22	15	93.8	287	2	BB309456
23	15	93.8	294	7	W40391
24	15	93.8	306	4	BI036238

25	15	93.8	310	2	BB251202
26	15	93.8	323	1	AI812549
27	15	93.8	338	1	AW921312
28	15	93.8	352	2	BP935524
29	15	93.8	365	7	CV001930
30	15	93.8	375	6	CB691996
31	15	93.8	394	6	CE698527
32	15	93.8	401	9	CE047936
33	15	93.8	408	4	BI536031
34	15	93.8	417	1	AA053186
35	15	93.8	419	5	BQ198462
36	15	93.8	423	1	AA147417
37	15	93.8	448	7	CN125873
38	15	93.8	455	6	CA902085
39	15	93.8	459	1	AA205003
40	15	93.8	465	8	B2180217
41	15	93.8	499	7	CF477353
42	15	93.8	502	9	CE812092
43	15	93.8	509	6	CA902086
44	15	93.8	511	4	BG982671
45	15	93.8	513	9	CE514588
46	15	93.8	514	9	CE258762
47	15	93.8	514	9	CE603007
48	15	93.8	515	4	BG691107
49	15	93.8	525	6	CA394047
50	15	93.8	530	8	AZ835303
51	15	93.8	542	6	CA193115
52	15	93.8	543	4	BM669271
53	15	93.8	548	4	BM717229
54	15	93.8	549	9	CL184460
55	15	93.8	551	4	BM693039
56	15	93.8	553	4	BJ676120
57	15	93.8	556	1	AA131157
58	15	93.8	565	1	AA121607
59	15	93.8	568	9	CE357759
60	15	93.8	575	2	BI187673
61	15	93.8	587	6	CA902088
62	15	93.8	588	7	CF669528
63	15	93.8	594	5	B0198426
64	15	93.8	604	9	CE041883
65	15	93.8	606	2	BE566668
66	15	93.8	606	4	BJ258115
67	15	93.8	607	8	AZ438519
68	15	93.8	608	6	CD733924
69	15	93.8	619	7	CF512619
70	15	93.8	623	9	CE304273
71	15	93.8	627	7	CF476778
72	15	93.8	627	9	CL412826
73	15	93.8	628	4	BG436842
74	15	93.8	639	6	CA293504
75	15	93.8	640	6	CD718076
76	15	93.8	640	6	CD719040
77	15	93.8	641	5	BU730169
78	15	93.8	651	6	CA145658
79	15	93.8	652	6	CA902087
80	15	93.8	662	6	CE333955
81	15	93.8	666	2	BB619841
82	15	93.8	666	4	BU263735
83	15	93.8	666	9	AG134513
84	15	93.8	669	6	CA191351
85	15	93.8	673	6	CA131063
86	15	93.8	674	6	CA817866
87	15	93.8	676	6	CA132259
88	15	93.8	676	9	CL601784
89	15	93.8	677	6	CD718015
90	15	93.8	680	6	CA190702
91	15	93.8	682	6	CA815948
92	15	93.8	694	4	CE214848
93	15	93.8	695	9	CR046007
94	15	93.8	707	6	CB339361
95	15	93.8	719	2	BB191088
96	15	93.8	720	9	CL574012
97	15	93.8	733	7	CV036218

BB251202	BB251202
AI812549	12G1_Pine
AW921312	ESR352616
BP935524	IL2-NT020
CV001930	G8A02-2m8
CB691996	AMGNNUC:S
CE698527	tlgr-g88-
CE047936	tlgr-g88-
BI536031	390188_MA
AA053186	2172404.r
BQ198462	NX1V131_E
AA147417	z03907.r
CN125873	RHOH1_13-
CA902085	PCSC10343
AA205003	z072e12.r
CA902086	tlgr-g88-
B2180217	CH230-485
CF477353	RTW3_7_B
CE812092	tlgr-g88-
CA902086	PCSC10343
BG982671	IL5-CN006
CE514588	tlgr-g88-
CE258762	tlgr-g88-
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99	15	93.8	749	6	CB341563	CB341563	172	14	87.5	249	6	CA539386	CA539386	C0278D06	C
100	15	93.8	749	6	CB982258	CB982258	172	14	87.5	253	9	CE010333	CE010333	LIgr-g8s-	C
101	15	93.8	752	4	BG386245	BG386245	173	14	87.5	256	9	CE525427	CE525427	AQ0692	SA
102	15	93.8	757	4	CD712674	CD712674	174	14	87.5	258	9	CE853225	CE853225	LIgr-g8s-	SA
103	15	93.8	758	5	BK909708	BK909708	175	14	87.5	259	9	CE853225	CE853225	LIgr-g8s-	SA
104	15	93.8	759	7	CF404762	CF404762	176	14	87.5	265	7	H34170	H34170	EST110813	R
105	15	93.8	761	7	CF664787	CF664787	177	14	87.5	266	1	BI064090	BI064090	tn57D07	X
106	15	93.8	762	9	CNS0158U	CNS0158U	178	14	87.5	266	1	BI064090	BI064090	tn57D07	X
107	15	93.8	768	8	B2612822	B2612822	179	14	87.5	275	5	AV085884	AV085884	AV085884	
108	15	93.8	769	6	CB341495	CB341495	180	14	87.5	280	1	AA778889	AA778889	2446812	8
109	15	93.8	771	6	CB342275	CB342275	181	14	87.5	285	7	CN310641	CN310641	170005318	
110	15	93.8	791	7	CF206902	CF206902	182	14	87.5	290	2	BF433605	BF433605	7455901	X
111	15	93.8	792	7	CF210957	CF210957	183	14	87.5	292	7	FI0815	FI0815	HSC3G082	n
112	15	93.8	797	7	CF210957	CF210957	184	14	87.5	297	7	FI0541	FI0541	HSC3G082	n
113	15	93.8	800	7	CO170582	CO170582	185	14	87.5	297	7	FI0541	FI0541	HSC3G082	n
114	15	93.8	801	5	BU107434	BU107434	186	14	87.5	297	7	FI0541	FI0541	HSC3G082	n
115	15	93.8	805	7	CO159063	CO159063	187	14	87.5	298	4	BF000628	BF000628	AT71803	X
116	15	93.8	808	7	CO368549	CO368549	188	14	87.5	298	4	BF000628	BF000628	AT71803	X
117	15	93.8	811	7	CF663301	CF663301	189	14	87.5	301	2	BE703009	BE703009	RC5-NN108	
118	15	93.8	815	7	CO247269	CO247269	190	14	87.5	301	2	BE703009	BE703009	RC5-NN108	
119	15	93.8	828	7	CK180837	CK180837	191	14	87.5	303	2	BF760650	BF760650	CMI-CT063	
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121	15	93.8	835	6	CL537542	CL537542	193	14	87.5	307	7	CL205193	CL205193	ZMBBD056	
122	15	93.8	848	7	CO367613	CO367613	194	14	87.5	308	9	CG648100	CG648100	OST400073	
123	15	93.8	852	2	BF137430	BF137430	195	14	87.5	320	6	CD610797	CD610797	56099586H	
124	15	93.8	853	2	BE563709	BE563709	196	14	87.5	321	5	BO570588	BO570588	51152402	
125	15	93.8	854	7	CF257869	CF257869	197	14	87.5	322	6	CD610798	CD610798	56099586U	
126	15	93.8	863	4	BG385624	BG385624	198	14	87.5	322	6	CD610798	CD610798	56099586U	
127	15	93.8	876	5	BU208515	BU208515	199	14	87.5	322	6	CD610798	CD610798	56099586U	
128	15	93.8	878	5	BO707838	BO707838	200	14	87.5	322	6	CD610798	CD610798	56099586U	
129	15	93.8	878	5	BO896349	BO896349	201	14	87.5	322	6	CD610798	CD610798	56099586U	
130	15	93.8	879	7	CO164380	CO164380	202	14	87.5	323	2	BE982287	BE982287	UI-M-CGDP	
131	15	93.8	884	1	AU067735	AU067735	203	14	87.5	324	1	BF092538	BF092538	0059F10	8
132	15	93.8	889	2	BE904092	BE904092	204	14	87.5	324	8	AZ037329	AZ037329	MR4-TN10	
133	15	93.8	890	4	BG386850	BG386850	205	14	87.5	325	1	AI886621	AI886621	tz59H06	X
134	15	93.8	910	5	BO943147	BO943147	206	14	87.5	332	5	BY052595	BY052595	CE271658	
135	15	93.8	963	5	BO943793	BO943793	207	14	87.5	332	5	BY052595	BY052595	CE271658	
136	15	93.8	977	5	BO932838	BO932838	208	14	87.5	332	5	BY052595	BY052595	CE271658	
137	15	93.8	977	5	BO678419	BO678419	209	14	87.5	334	7	H29468	H29468	LIgr-g8s-	
138	15	93.8	984	5	CL065453	CL065453	210	14	87.5	335	1	AA169875	AA169875	Ym26E11	81
139	15	93.8	1031	9	CL083700	CL083700	211	14	87.5	336	1	AA169875	AA169875	Ym26E11	81
140	15	93.8	1034	5	BQ054522	BQ054522	212	14	87.5	338	1	AA437792	AA437792	ve33F02	X
141	15	93.8	1091	8	CC212299	CC212299	213	14	87.5	340	1	AA628691	AA628691	af30G06	8
142	15	93.8	1111	8	CC194571	CC194571	214	14	87.5	341	1	AA628691	AA628691	af30G06	8
143	15	93.8	1184	6	CD507034	CD507034	215	14	87.5	342	5	AA328838	AA328838	EST32582	
144	15	93.8	1768	4	BP65185	BP65185	216	14	87.5	342	5	BY318311	BY318311	EST32582	
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146	15	93.8	2637	3	AK039581	AK039581	218	14	87.5	344	1	AI648372	AI648372	tx51h08	X
147	15	93.8	2700	3	AK038354	AK038354	219	14	87.5	350	5	BY128036	BY128036	56099593H	
148	15	93.8	2767	3	AK030869	AK030869	220	14	87.5	355	9	CE669297	CE669297	LIgr-g8s-	
149	15	93.8	4880	3	HSMB07270	HSMB07270	221	14	87.5	355	5	BY028627	BY028627	LIgr-g8s-	
150	15	93.8	97	7	CV307039	CV307039	222	14	87.5	355	7	BY028627	BY028627	LIgr-g8s-	
151	15	93.8	97	7	CV307039	CV307039	223	14	87.5	355	7	BY028627	BY028627	LIgr-g8s-	
152	15	93.8	115	7	BE574999	BE574999	224	14	87.5	361	1	AI767922	AI767922	w199D10	81
153	15	93.8	123	6	CD953550	CD953550	225	14	87.5	361	1	AI767922	AI767922	w199D10	81
154	15	93.8	134	6	CD953550	CD953550	226	14	87.5	369	5	BY023082	BY023082	YX22805	81
155	15	93.8	143	6	CL315386	CL315386	227	14	87.5	371	7	N35328	N35328	wc21912	X
156	15	93.8	155	4	BF947018	BF947018	228	14	87.5	375	1	AI688774	AI688774	6099593J	
157	15	93.8	162	8	AZ033179	AZ033179	229	14	87.5	375	6	BY053435	BY053435	56099593H	
158	15	93.8	176	1	AA014726	AA014726	230	14	87.5	377	6	CD610799	CD610799	56099593H	
159	15	93.8	182	1	AA008345	AA008345	231	14	87.5	377	6	CD610799	CD610799	56099593H	
160	15	93.8	187	4	BI320436	BI320436	232	14	87.5	379	6	CD610799	CD610799	56099593H	
161	15	93.8	188	4	CE754117	CE754117	233	14	87.5	380	5	BU050329	BU050329	1679F10	X
162	15	93.8	197	6	CD954678	CD954678	234	14	87.5	381	1	AI191606	AI191606	q662A10	X
163	15	93.8	198	6	CD942263	CD942263	235	14	87.5	381	1	AI191606	AI191606	q662A10	X
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165	15	93.8	198	6	CD953580	CD953580	237	14	87.5	381	1	AI191606	AI191606	q662A10	X
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168	15	93.8	198	6	CD954914	CD954914	240	14	87.5	382	1	AI165598	AI165598	A086D73u	
169	15	93.8	198	6	CD955746	CD955746	241	14	87.5	384	6	BY577264	BY577264	BY577264	
170	15	93.8	198	6	CD965469	CD965469	242	14	87.5	386	6	BY087937	BY087937	BY087937	
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244	14	87.5	387	5	BY394941	BY394941	BY394941	317	14	87.5	458	5	BY263437	BY263437	BY263437
245	14	87.5	387	7	CO991172	CO991172	CO991172	318	14	87.5	459	1	AI086454	AI086454	AI086454
246	14	87.5	388	1	AI892460	AI892460	AI892460	319	14	87.5	459	1	AJ775688	AJ775688	AJ775688
247	14	87.5	388	4	BI257648	BI257648	BI257648	320	14	87.5	459	9	CE657978	CE657978	CE657978
248	14	87.5	392	1	AI358608	AI358608	AI358608	321	14	87.5	460	8	BH223284	BH223284	BH223284
249	14	87.5	392	2	BE702990	BE702990	BE702990	322	14	87.5	462	5	BU972697	BU972697	BU972697
250	14	87.5	392	5	BY308861	BY308861	BY308861	323	14	87.5	462	6	CF009087	CF009087	CF009087
251	14	87.5	392	9	CE458523	CE458523	CE458523	324	14	87.5	463	2	BE671703	BE671703	BE671703
252	14	87.5	393	6	AO852858	AO852858	AO852858	325	14	87.5	464	1	AA014339	AA014339	AA014339
253	14	87.5	396	6	BY578602	BY578602	BY578602	326	14	87.5	464	1	AI858784	AI858784	AI858784
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255	14	87.5	398	9	CE510041	CE510041	CE510041	328	14	87.5	464	9	CE255220	CE255220	CE255220
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257	14	87.5	404	2	AM168328	AM168328	AM168328	330	14	87.5	467	2	BE677543	BE677543	BE677543
258	14	87.5	404	5	BY264309	BY264309	BY264309	331	14	87.5	467	6	CD874254	CD874254	CD874254
259	14	87.5	405	6	CB811230	CB811230	CB811230	332	14	87.5	468	2	BE049449	BE049449	BE049449
260	14	87.5	406	6	CA004036	CA004036	CA004036	333	14	87.5	469	1	AI923515	AI923515	AI923515
261	14	87.5	407	8	BO3161	BO3161	BO3161	334	14	87.5	469	9	CE096790	CE096790	CE096790
262	14	87.5	409	9	CE448084	CE448084	CE448084	335	14	87.5	470	1	AI153827	AI153827	AI153827
263	14	87.5	411	1	AI260456	AI260456	AI260456	336	14	87.5	470	2	AM182781	AM182781	AM182781
264	14	87.5	411	1	AI590639	AI590639	AI590639	337	14	87.5	471	7	R56230	R56230	R56230
265	14	87.5	412	5	BY056345	BY056345	BY056345	338	14	87.5	471	9	CE542973	CE542973	CE542973
266	14	87.5	412	7	W68959	W68959	W68959	339	14	87.5	471	9	BO901314	BO901314	BO901314
267	14	87.5	412	7	W62003	W62003	W62003	340	14	87.5	472	5	BO901314	BO901314	BO901314
268	14	87.5	413	2	BF511227	BF511227	BF511227	341	14	87.5	473	5	BQ112058	BQ112058	BQ112058
269	14	87.5	414	1	AI087128	AI087128	AI087128	342	14	87.5	475	1	AA259368	AA259368	AA259368
270	14	87.5	414	2	BE326871	BE326871	BE326871	343	14	87.5	475	7	R90558	R90558	R90558
271	14	87.5	416	1	AA644522	AA644522	AA644522	344	14	87.5	476	5	BY365943	BY365943	BY365943
272	14	87.5	417	5	BY270421	BY270421	BY270421	345	14	87.5	476	1	AA485525	AA485525	AA485525
273	14	87.5	417	9	CE306559	CE306559	CE306559	346	14	87.5	478	9	CE615388	CE615388	CE615388
274	14	87.5	418	1	AA678335	AA678335	AA678335	347	14	87.5	481	1	AA106048	AA106048	AA106048
275	14	87.5	418	1	AI871070	AI871070	AI871070	348	14	87.5	481	2	AM085524	AM085524	AM085524
276	14	87.5	418	2	BE688256	BE688256	BE688256	349	14	87.5	483	8	AZ877835	AZ877835	AZ877835
277	14	87.5	418	5	BY486629	BY486629	BY486629	350	14	87.5	483	9	CG671517	CG671517	CG671517
278	14	87.5	419	7	W12858	W12858	W12858	351	14	87.5	488	1	AA974025	AA974025	AA974025
279	14	87.5	420	1	AA407226	AA407226	AA407226	352	14	87.5	488	1	AQ0880025	AQ0880025	AQ0880025
280	14	87.5	420	1	AI325772	AI325772	AI325772	353	14	87.5	491	1	AA927654	AA927654	AA927654
281	14	87.5	422	1	AJ710865	AJ710865	AJ710865	354	14	87.5	491	1	AJ779076	AJ779076	AJ779076
282	14	87.5	423	5	BO599722	BO599722	BO599722	355	14	87.5	491	5	BX645203	BX645203	BX645203
283	14	87.5	423	6	CA809864	CA809864	CA809864	356	14	87.5	491	5	BY495357	BY495357	BY495357
284	14	87.5	425	1	AA407137	AA407137	AA407137	357	14	87.5	491	9	CC830864	CC830864	CC830864
285	14	87.5	426	8	BO2789	BO2789	BO2789	358	14	87.5	492	1	AA014622	AA014622	AA014622
286	14	87.5	427	5	BY430071	BY430071	BY430071	359	14	87.5	492	7	CN310637	CN310637	CN310637
287	14	87.5	429	2	BE500981	BE500981	BE500981	360	14	87.5	492	8	BH269485	BH269485	BH269485
288	14	87.5	429	6	CA568751	CA568751	CA568751	361	14	87.5	493	7	CE492773	CE492773	CE492773
289	14	87.5	430	1	AA033054	AA033054	AA033054	362	14	87.5	496	7	CF907776	CF907776	CF907776
290	14	87.5	430	7	W64958	W64958	W64958	363	14	87.5	497	6	CD923425	CD923425	CD923425
291	14	87.5	433	5	BY505197	BY505197	BY505197	364	14	87.5	498	1	AA466023	AA466023	AA466023
292	14	87.5	433	8	AZ586226	AZ586226	AZ586226	365	14	87.5	498	2	BE234847	BE234847	BE234847
293	14	87.5	435	2	AO813525	AO813525	AO813525	366	14	87.5	498	6	CA561977	CA561977	CA561977
294	14	87.5	436	1	AI817667	AI817667	AI817667	367	14	87.5	498	6	CA656757	CA656757	CA656757
295	14	87.5	436	2	AW468996	AW468996	AW468996	368	14	87.5	499	2	BE851236	BE851236	BE851236
296	14	87.5	437	7	W89731	W89731	W89731	369	14	87.5	499	9	CE551084	CE551084	CE551084
297	14	87.5	437	9	CR303758	CR303758	CR303758	370	14	87.5	500	2	BE195700	BE195700	BE195700
298	14	87.5	438	2	AM136487	AM136487	AM136487	371	14	87.5	504	8	AQ033160	AQ033160	AQ033160
299	14	87.5	440	2	BB859094	BB859094	BB859094	372	14	87.5	505	8	AO455482	AO455482	AO455482
300	14	87.5	441	1	AI859818	AI859818	AI859818	373	14	87.5	508	4	BG144799	BG144799	BG144799
301	14	87.5	442	8	AO533984	AO533984	AO533984	374	14	87.5	508	5	BY158097	BY158097	BY158097
302	14	87.5	445	5	AM139790	AM139790	AM139790	375	14	87.5	510	1	AI1994130	AI1994130	AI1994130
303	14	87.5	445	8	BH858855	BH858855	BH858855	376	14	87.5	515	6	CD843769	CD843769	CD843769
304	14	87.5	447	2	AM206554	AM206554	AM206554	377	14	87.5	516	7	CF842185	CF842185	CF842185
305	14	87.5	447	9	CE185855	CE185855	CE185855	378	14	87.5	520	2	BF001816	BF001816	BF001816
306	14	87.5	447	9	CE185855	CE185855	CE185855	379	14	87.5	520	1	AI564801	AI564801	AI564801
307	14	87.5	450	2	AM294117	AM294117	AM294117	380	14	87.5	520	1	AI885151	AI885151	AI885151
308	14	87.5	450	2	BE109612	BE109612	BE109612	381	14	87.5	520	2	BF055065	BF055065	BF055065
309	14	87.5	452	1	AI655930	AI655930	AI655930	382	14	87.5	520	9	CE617994	CE617994	CE617994
310	14	87.5	454	2	AM206668	AM206668	AM206668	383	14	87.5	521	1	AA261718	AA261718	AA261718
311	14	87.5	454	5	BY277268	BY277268	BY277268	384	14	87.5	521	5	BQ832749	BQ832749	BQ832749
312	14	87.5	455	7	CE294659	CE294659	CE294659	385	14	87.5	521	5	BQ832749	BQ832749	BQ832749
313	14	87.5	455	7	R85051	R85051	R85051	386	14	87.5	521	5	BQ832749	BQ832749	BQ832749
314	14	87.5	456	6	CA559676	CA559676	CA559676	387	14	87.5	521	5	BQ832749	BQ832749	BQ832749
315	14	87.5	457	1	AI225804	AI225804	AI225804	388	14	87.5	521	5	BQ832749	BQ832749	BQ832749
316	14	87.5	457	1	AI225804	AI225804	AI225804	389	14	87.5	521	5	BQ832749	BQ832749	BQ832749

390	14	87.5	521	5	BU734867	UI-E-DW0-	463	14	87.5	580	5	BQ901430	BQ901430	Ta02_19f0
391	14	87.5	523	2	BF433551	BF433551	464	14	87.5	580	5	BQ902421	BQ902421	Ta02_02a0
392	14	87.5	524	9	CE189596	CE189596	465	14	87.5	581	5	BP252648	BP252648	BP252648
393	14	87.5	526	1	AI527345	AI527345	466	14	87.5	581	5	BQ902063	BQ902063	Ta02_07h0
394	14	87.5	527	2	BF594824	BF594824	467	14	87.5	582	2	AW101904	AW101904	Ba72C05.Y
395	14	87.5	527	2	AM190802	AM190802	468	14	87.5	582	5	BP271039	BP271039	BP271039
396	14	87.5	529	7	CE674419	CE674419	469	14	87.5	582	5	BP288264	BP288264	BP288264
397	14	87.5	529	7	CO595580	CO595580	470	14	87.5	582	5	BP361364	BP361364	BP361364
398	14	87.5	529	7	CR175354	CR175354	471	14	87.5	583	2	AM964954	AM964954	EST376922
399	14	87.5	530	1	AL629513	AL629513	472	14	87.5	584	6	CD293216	CD293216	SRTPU536.
400	14	87.5	531	6	CA603741	CA603741	473	14	87.5	586	1	AD145824	AD145824	ME68C11.T
401	14	87.5	532	2	AV548987	AV548987	474	14	87.5	586	8	BH067631	BH067631	RPCI-24-2
402	14	87.5	532	2	BE591432	BE591432	475	14	87.5	586	9	AG362240	AG362240	MUS mUSCU
403	14	87.5	532	7	HI7628	HI7628	476	14	87.5	587	1	AA141444	AA141444	CK01811.5
404	14	87.5	534	7	CV355785	CV355785	477	14	87.5	587	1	AU056398	AU056398	AU056398
405	14	87.5	535	6	CB718072	CB718072	478	14	87.5	587	4	BM250087	BM250087	K0844B06-
406	14	87.5	535	8	AQ558246	AQ558246	479	14	87.5	587	5	BQ295332	BQ295332	WHE2869_E
407	14	87.5	536	9	CE590031	CE590031	480	14	87.5	588	9	CE285790	CE285790	LtGr-g88-
408	14	87.5	537	1	AI603779	AI603779	481	14	87.5	589	6	CD615344	CD615344	56050733H
409	14	87.5	538	2	BF057394	BF057394	482	14	87.5	589	6	CD615345	CD615345	56050733J
410	14	87.5	538	2	CB717477	CB717477	483	14	87.5	589	7	W31110	W31110	zb85f12.r1
411	14	87.5	539	9	CE850654	CE850654	484	14	87.5	591	1	AI464863	AI464863	ME92d01.Y
412	14	87.5	541	5	BQ901739	BQ901739	485	14	87.5	591	6	CAS60747	CAS60747	K0276G05-
413	14	87.5	541	7	CO684801	CO684801	486	14	87.5	591	9	CE379196	CE379196	LtGr-g88-
414	14	87.5	541	9	CE678435	CE678435	487	14	87.5	595	2	BF494674	BF494674	AT03379..5
415	14	87.5	542	2	BE244521	BE244521	488	14	87.5	596	6	CA019764	CA019764	HV13A18x
416	14	87.5	542	5	BO620649	BO620649	489	14	87.5	596	6	CD997943	CD997943	OR85e10.X
417	14	87.5	542	7	CF857710	CF857710	490	14	87.5	597	9	CE139460	CE139460	LtGr-g88-
418	14	87.5	543	1	AI111725	AI111725	491	14	87.5	598	2	BF462217	BF462217	WHE1798_B
419	14	87.5	546	1	AI571347	AI571347	492	14	87.5	598	2	BE978594	BE978594	Ba80f02.Y
420	14	87.5	547	1	AI563989	AI563989	493	14	87.5	598	6	CA696693	CA696693	W1K8.PK0
421	14	87.5	547	2	BF722838	BF722838	494	14	87.5	600	4	BI987687	BI987687	3204-.58 M
422	14	87.5	548	1	AI610456	AI610456	495	14	87.5	600	9	CE137159	CE137159	LtGr-g88-
423	14	87.5	548	1	AI610642	AI610642	496	14	87.5	600	9	CE233377	CE233377	LtGr-g88-
424	14	87.5	549	5	BQ901379	BQ901379	497	14	87.5	601	9	CE388330	CE388330	LtGr-g88-
425	14	87.5	550	5	BQ017394	BQ017394	498	14	87.5	601	9	CE575207	CE575207	LtGr-g88-
426	14	87.5	551	8	AZ440782	AZ440782	499	14	87.5	603	9	CE243209	CE243209	LtGr-g88-
427	14	87.5	552	1	AU143957	AU143957	500	14	87.5	603	9	CE650456	CE650456	LtGr-g88-
428	14	87.5	552	7	CF906006	CF906006	501	14	87.5	604	9	CE723170	CE723170	LtGr-g88-
429	14	87.5	553	1	AV406141	AV406141	502	14	87.5	604	9	CE793923	CE793923	LtGr-g88-
430	14	87.5	554	6	CA701608	CA701608	503	14	87.5	605	2	BE310003	BE310003	LtGr-g88-
431	14	87.5	555	2	CM011371	CM011371	504	14	87.5	606	9	CE351120	CE351120	LtGr-g88-
432	14	87.5	556	4	BG057682	BG057682	505	14	87.5	607	2	BE853348	BE853348	3-5D-MY P
433	14	87.5	556	9	CE105609	CE105609	506	14	87.5	607	4	BG087199	BG087199	H3136G01-
434	14	87.5	557	7	CF982293	CF982293	507	14	87.5	608	8	AZ306456	AZ306456	IM0007J04
435	14	87.5	558	1	AA148045	AA148045	508	14	87.5	609	4	BG319748	BG319748	ZM03_0591
436	14	87.5	558	7	CM008833	CM008833	509	14	87.5	609	7	CF904382	CF904382	A0421F09-
437	14	87.5	559	9	CE804967	CE804967	510	14	87.5	609	8	BZ420678	BZ420678	IF70903.B
438	14	87.5	560	5	BU726819	BU726819	511	14	87.5	611	1	AI625072	AI625072	L649e01.X
439	14	87.5	560	6	CD635565	CD635565	512	14	87.5	611	9	CE193885	CE193885	LtGr-g88-
440	14	87.5	560	7	CF725721	CF725721	513	14	87.5	612	1	AA877325	AA877325	MT01a01.6
441	14	87.5	562	7	CK368980	CK368980	514	14	87.5	613	7	CK347000	CK347000	L0944F06-
442	14	87.5	564	4	BM255235	BM255235	515	14	87.5	615	6	CB272602	CB272602	MT160606.
443	14	87.5	565	7	CK966170	CK966170	516	14	87.5	616	5	BM590753	BM590753	BM590753
444	14	87.5	566	2	BF051295	BF051295	517	14	87.5	616	6	CA646838	CA646838	Wre1n.PK0
445	14	87.5	567	7	CF204432	CF204432	518	14	87.5	616	9	CE447347	CE447347	LtGr-g88-
446	14	87.5	567	7	CF904296	CF904296	519	14	87.5	617	1	AA118127	AA118127	MT10010.1
447	14	87.5	567	9	CE9041433	CE9041433	520	14	87.5	617	2	BB634100	BB634100	BB634100
448	14	87.5	567	9	CE359144	CE359144	521	14	87.5	617	2	BE867183	BE867183	WHE0519_D
449	14	87.5	568	2	BE860598	BE860598	522	14	87.5	618	7	CV242969	CV242969	W602516.B
450	14	87.5	568	4	BG299616	BG299616	523	14	87.5	620	2	BB619902	BB619902	BB619902
451	14	87.5	570	2	BE592057	BE592057	524	14	87.5	620	6	CA318800	CA318800	UT-M-FV0-
452	14	87.5	571	1	AI611045	AI611045	525	14	87.5	622	9	CE007950	CE007950	LtGr-g88-
453	14	87.5	574	2	CC705994	CC705994	526	14	87.5	624	2	BE987294	BE987294	UT-M-CG0P
454	14	87.5	575	2	BF499789	BF499789	527	14	87.5	624	6	CD058164	CD058164	HO051215
455	14	87.5	575	6	BY600207	BY600207	528	14	87.5	625	6	CB522815	CB522815	UT-M-GK0-
456	14	87.5	575	9	CE203653	CE203653	529	14	87.5	626	8	CE188014	CE188014	LtGr-g88-
457	14	87.5	575	9	CL383415	CL383415	530	14	87.5	626	8	BZ993811	BZ993811	PDDU76TD
458	14	87.5	576	7	CF893982	CF893982	531	14	87.5	627	7	CO588717	CO588717	DG2-2395
459	14	87.5	578	2	CE539687	CE539687	532	14	87.5	628	2	BB616651	BB616651	BB616651
460	14	87.5	579	2	AM939913	AM939913	533	14	87.5	629	1	AI412007	AI412007	EST240301
461	14	87.5	579	5	BQ902333	BQ902333	534	14	87.5	629	2	AM536490	AM536490	GO105B03-
462	14	87.5	579	5	BU741019	BU741019	535	14	87.5	629	5	BM984803	BM984803	UT-CF-EC1

536	14	87.5	630	6	CD9311767	CD9311767	GR45.1151	609	14	87.5	698	9	CE622321	CE622321	t1gr-g88-
537	14	87.5	632	8	B2138683	B2138683	CH230-387	610	14	87.5	699	2	BF497217	BF497217	BF497217
538	14	87.5	632	8	B2642803	B2642803	OGA0697C	611	14	87.5	699	2	BF984241	BF984241	BF984241
539	14	87.5	633	1	AV826345	AV826345	AV826345	612	14	87.5	700	7	CK567115	CK567115	CK567115
540	14	87.5	634	1	EM971609	EM971609	UI-CF-EC1	613	14	87.5	702	5	B0633147	B0633147	B0633147
541	14	87.5	634	6	CA029583	CA029583	H265K03x	614	14	87.5	703	5	B0008775	B0008775	B0008775
542	14	87.5	637	8	A2269017	A2269017	RPCI-23-1	615	14	87.5	703	7	CF634435	CF634435	CF634435
543	14	87.5	638	9	CE415077	CE415077	t1gr-g88-	616	14	87.5	704	7	CO247483	CO247483	CO247483
544	14	87.5	639	2	BB204409	BB204409	BB204409	617	14	87.5	706	5	B0000856	B0000856	B0000856
545	14	87.5	640	9	CR254497	CR254497	Reverse	618	14	87.5	706	5	BX504413	BX504413	BX504413
546	14	87.5	641	7	CF905263	CF905263	A0432D08-	619	14	87.5	706	8	B2546589	B2546589	B2546589
547	14	87.5	644	5	BQ747303	BQ747303	UI-M-PA0-	620	14	87.5	707	9	CE728433	CE728433	CE728433
548	14	87.5	645	6	CA196182	CA196182	SCSBAD108	621	14	87.5	710	5	BM980924	BM980924	BM980924
549	14	87.5	645	9	CC767705	CC767705	CH240.66D	622	14	87.5	710	6	CA423554	CA423554	CA423554
550	14	87.5	645	9	CE573905	CE573905	t1gr-g88-	623	14	87.5	710	6	CA427124	CA427124	CA427124
551	14	87.5	646	2	BB598293	BB598293	BB598293	624	14	87.5	712	9	CNS05P29	CNS05P29	CNS05P29
552	14	87.5	646	5	BQ446812	BQ446812	UI-H-EU1-	625	14	87.5	713	6	BY753072	BY753072	BY753072
553	14	87.5	646	5	B0732265	B0732265	UI-E-CQ1-	626	14	87.5	714	9	CR143208	CR143208	CR143208
554	14	87.5	646	6	CA311297	CA311297	UI-H-DE1-	627	14	87.5	715	9	CNS03SVQ	CNS03SVQ	CNS03SVQ
555	14	87.5	646	6	CA436361	CA436361	UI-H-DE1-	628	14	87.5	715	9	CE213328	CE213328	CE213328
556	14	87.5	649	5	BU631088	BU631088	UI-H-PE1-	629	14	87.5	716	2	BF608303	BF608303	BF608303
557	14	87.5	649	6	CD927206	CD927206	GR45.101E	630	14	87.5	716	5	BM981155	BM981155	BM981155
558	14	87.5	650	7	CP294881	CP294881	30DG5--04	631	14	87.5	716	5	BQ194023	BQ194023	BQ194023
559	14	87.5	650	7	CV006340	CV006340	CS_g11_14	632	14	87.5	721	6	BF346081	BF346081	BF346081
560	14	87.5	651	4	BA548742	BA548742	BA548742	633	14	87.5	721	2	CNS05P50	CNS05P50	CNS05P50
561	14	87.5	653	1	AA876227	AA876227	nx25h01.8	634	14	87.5	721	8	AZ250654	AZ250654	AZ250654
562	14	87.5	653	6	CD931180	CD931180	GR45.113L	635	14	87.5	722	8	AG485283	AG485283	AG485283
563	14	87.5	654	6	CD931181	CD931181	GR45.113L	636	14	87.5	723	1	AL110416	AL110416	AL110416
564	14	87.5	655	7	CP631327	CP631327	zmtw948_0	637	14	87.5	725	1	BM971334	BM971334	BM971334
565	14	87.5	657	2	BF488258	BF488258	AT23485.5	638	14	87.5	727	5	CE409035	CE409035	CE409035
566	14	87.5	657	7	CF902322	CF902322	A0339C06-	639	14	87.5	727	9	CE405999	CE405999	CE405999
567	14	87.5	658	5	B0004401	B0004401	UI-H-E10-	640	14	87.5	728	6	B1598138	B1598138	B1598138
568	14	87.5	658	6	CB600291	CB600291	AGENCOURT	641	14	87.5	728	6	CD240976	CD240976	CD240976
569	14	87.5	660	6	BY753686	BY753686	BY753686	642	14	87.5	730	9	CC512431	CC512431	CC512431
570	14	87.5	660	6	CA216538	CA216538	SCCFL500	643	14	87.5	730	9	BF488931	BF488931	BF488931
571	14	87.5	661	6	BB624945	BB624945	BB624945	644	14	87.5	731	2	CK474134	CK474134	CK474134
572	14	87.5	662	2	BY753487	BY753487	BY753487	645	14	87.5	731	7	CK476841	CK476841	CK476841
573	14	87.5	663	6	CA135166	CA135166	SCFLRT101	646	14	87.5	733	7	CO430874	CO430874	CO430874
574	14	87.5	663	7	CR413421	CR413421	CR413421	647	14	87.5	734	9	CNS05N28	CNS05N28	CNS05N28
575	14	87.5	668	1	AL042531	AL042531	DKZP2434H	648	14	87.5	736	9	CC493248	CC493248	CC493248
576	14	87.5	670	7	CN280352	CN280352	1700P5319	649	14	87.5	738	5	BQ207080	BQ207080	BQ207080
577	14	87.5	671	1	AI048249	AI048249	ud71f08.Y	650	14	87.5	738	5	CE817615	CE817615	CE817615
578	14	87.5	671	2	BE975003	BE975003	bs37e09.Y	651	14	87.5	739	4	BG064967	BG064967	BG064967
579	14	87.5	671	6	BY753431	BY753431	BY753431	652	14	87.5	740	7	CN221047	CN221047	CN221047
580	14	87.5	671	6	CN280354	CN280354	1700P5336	653	14	87.5	740	2	BF791564	BF791564	BF791564
581	14	87.5	671	7	CN295840	CN295840	1700P5325	654	14	87.5	744	2	BF494210	BF494210	BF494210
582	14	87.5	676	5	BU609825	BU609825	UI-M-DJ2-	655	14	87.5	744	6	CB601577	CB601577	CB601577
583	14	87.5	677	1	AI405290	AI405290	GH25245.5	656	14	87.5	744	9	AG372210	AG372210	AG372210
584	14	87.5	677	9	CE451616	CE451616	t1gr-g88-	657	14	87.5	745	4	B1751593	B1751593	B1751593
585	14	87.5	677	9	CE575299	CE575299	t1gr-g88-	658	14	87.5	746	1	AA986905	AA986905	AA986905
586	14	87.5	677	9	CE575299	CE575299	t1gr-g88-	659	14	87.5	746	9	CNS056MT	CNS056MT	CNS056MT
587	14	87.5	677	9	CE630847	CE630847	t1gr-g88-	660	14	87.5	747	7	CV077937	CV077937	CV077937
588	14	87.5	679	5	BU615358	BU615358	UI-H-FH0-	661	14	87.5	749	4	BG416135	BG416135	BG416135
589	14	87.5	680	7	CO043288	CO043288	UI-M-EH0P	662	14	87.5	749	5	BM945422	BM945422	BM945422
590	14	87.5	681	9	CE218664	CE218664	t1gr-g88-	663	14	87.5	749	7	CO403404	CO403404	CO403404
591	14	87.5	681	9	BE503046	BE503046	RT18948.5	664	14	87.5	750	5	BU239867	BU239867	BU239867
592	14	87.5	682	8	AO415326	AO415326	RPCI-11-1	665	14	87.5	750	5	BU633698	BU633698	BU633698
593	14	87.5	684	6	BY754188	BY754188	BY754188	666	14	87.5	751	5	BQ209397	BQ209397	BQ209397
594	14	87.5	684	9	CE210238	CE210238	t1gr-g88-	667	14	87.5	751	7	CO568111	CO568111	CO568111
595	14	87.5	684	9	CE755791	CE755791	t1gr-g88-	668	14	87.5	752	6	CA321509	CA321509	CA321509
596	14	87.5	686	4	BM078495	BM078495	MEST130-MA	669	14	87.5	758	7	CF955237	CF955237	CF955237
597	14	87.5	686	6	CB454191	CB454191	710912.0D	670	14	87.5	758	8	B2096470	B2096470	B2096470
598	14	87.5	687	7	CO597351	CO597351	DG8-145b7	671	14	87.5	757	5	BQ205282	BQ205282	BQ205282
599	14	87.5	688	7	CO684084	CO684084	DG11-1780	672	14	87.5	767	6	CB572909	CB572909	CB572909
600	14	87.5	688	7	BQ263553	BQ263553	BY753761	673	14	87.5	771	4	BF969066	BF969066	BF969066
601	14	87.5	690	6	BY753761	BY753761	BY753761	674	14	87.5	772	6	CB238171	CB238171	CB238171
602	14	87.5	694	6	BG435548	BG435548	602508174	675	14	87.5	776	4	BG923868	BG923868	BG923868
603	14	87.5	696	6	BY762798	BY762798	BY762798	676	14	87.5	777	4	BG245752	BG245752	BG245752
604	14	87.5	696	8	AQ380435	AQ380435	RPCI11-16	677	14	87.5	778	8	B05083	B05083	B05083
605	14	87.5	697	4	BI753342	BI753342	603026507	678	14	87.5	778	9	CE233274	CE233274	CE233274
606	14	87.5	697	4	CA422848	CA422848	UI-H-PE1-	679	14	87.5	779	7	CN458776	CN458776	CN458776
607	14	87.5	697	6	CA431599	CA431599	UI-H-FG1-	680	14	87.5	779	7	BG976173	BG976173	BG976173
608	14	87.5	697	6	CA431599	CA431599	UI-H-FG1-	681	14	87.5	782	4	BG976173	BG976173	BG976173
609	14	87.5	698	9	CE622321	CE622321	t1gr-g88-	698	14	87.5	782	4	BG976173	BG976173	BG976173
610	14	87.5	699	2	BF497217	BF497217	BF497217	699	14	87.5	782	4	BG976173	BG976173	BG976173
611	14	87.5	699	2	BF984241	BF984241	BF984241	700	14	87.5	782	4	BG976173	BG976173	BG976173
612	14	87.5	700	7	CK567115	CK567115	CK567115	701	14	87.5	782	4	BG976173	BG976173	BG976173
613	14	87.5	702	5	B0633147	B0633147	B0633147	702	14	87.5	782	4	BG976173	BG976173	BG976173
614	14	87.5	703	5	B0008775	B0008775	B0008775	703	14	87.5	782	4	BG976173	BG976173	BG976173
615	14	87.5	703	7	CF634435	CF634435	CF634435	704	14	87.5	782	4	BG976173	BG976173	BG976173
616	14	87.5	704	7</											

C 682	14	87.5	785	5	BUR38811	AGENCOURT	C 755	14	87.5	914	7	CKI60279	FGAS0418
C 683	14	87.5	785	5	AG305561	HUB_mubcu	C 756	14	87.5	917	5	BQ710323	AGENCOURT
C 684	14	87.5	787	2	BF267052	HY_CEA001	C 757	14	87.5	918	5	BQ710334	AGENCOURT
C 685	14	87.5	787	2	BF496165	AT09894.5	C 758	14	87.5	919	5	BK456183	EX456183
C 686	14	87.5	788	2	BF506017	AT08366.5	C 759	14	87.5	921	4	BG754328	BG754328
C 687	14	87.5	788	4	B1760288	603045353	C 760	14	87.5	921	5	BQ711247	CF582656
C 688	14	87.5	790	4	BG847553	1024017H1	C 761	14	87.5	921	7	CF582656	AGENCOURT
C 689	14	87.5	793	6	CB602173	AGENCOURT	C 762	14	87.5	925	6	CD359022	AGENCOURT
C 690	14	87.5	798	7	CK476826	AGENCOURT	C 763	14	87.5	926	4	BG761406	CG405087
C 691	14	87.5	803	5	BUS61785	AGENCOURT	C 764	14	87.5	927	8	CG405087	CG405087
C 692	14	87.5	808	9	BX180023	Danlo_rer	C 765	14	87.5	927	9	CL027706	CL027706
C 693	14	87.5	809	1	AU079824	AU079824	C 766	14	87.5	928	9	CG316604	CG316604
C 694	14	87.5	809	5	BX102623	Reverse_8	C 767	14	87.5	928	9	CL061017	CL061017
C 695	14	87.5	810	9	CR135688	Reverse_8	C 768	14	87.5	929	4	B1558719	B1558719
C 696	14	87.5	811	7	BE382952	AGENCOURT	C 769	14	87.5	933	5	BQ228431	BQ228431
C 697	14	87.5	811	7	CK478486	AGENCOURT	C 770	14	87.5	936	5	BQ228431	BQ228431
C 698	14	87.5	821	6	CA473760	AGENCOURT	C 771	14	87.5	937	9	CNS05KIC	CNS05KIC
C 699	14	87.5	823	7	CK198465	FGAS00695	C 772	14	87.5	942	5	BQ712604	BQ712604
C 700	14	87.5	831	9	CNS0124H	AGENCOURT	C 773	14	87.5	942	5	BUS10688	BUS10688
C 701	14	87.5	831	6	B1454760	603172572	C 774	14	87.5	947	5	BQ918897	BQ918897
C 702	14	87.5	831	6	CA194529	SCVPS106	C 775	14	87.5	947	5	BUS98623	BUS98623
C 703	14	87.5	832	2	BF383361	602045022	C 776	14	87.5	949	9	CG270680	CG270680
C 704	14	87.5	837	4	BG117202	602346481	C 777	14	87.5	951	4	BG172230	BG172230
C 705	14	87.5	838	5	BQ710702	AGENCOURT	C 778	14	87.5	954	2	BE213711	BE213711
C 706	14	87.5	839	5	BF256481	HYSMEE001	C 779	14	87.5	958	2	BF793052	BF793052
C 707	14	87.5	839	5	BQ889770	AGENCOURT	C 780	14	87.5	962	4	B1692831	B1692831
C 708	14	87.5	840	9	CF932841	TREB-T-B04	C 781	14	87.5	970	9	CNS05782	CNS05782
C 709	14	87.5	842	9	CC532607	CH240_410	C 782	14	87.5	972	1	AL542558	AL542558
C 710	14	87.5	845	4	B1409559	602963988	C 783	14	87.5	972	1	CG044755	CG044755
C 711	14	87.5	847	6	CB988872	AGENCOURT	C 784	14	87.5	975	9	CNS05SRA	CNS05SRA
C 712	14	87.5	847	7	CK196957	FGAS00542	C 785	14	87.5	977	9	CG264088	CG264088
C 713	14	87.5	851	6	CA466806	AGENCOURT	C 786	14	87.5	978	2	BE533136	BE533136
C 714	14	87.5	851	6	CG044757	PURCOS4TD	C 787	14	87.5	979	9	CL031650	CL031650
C 715	14	87.5	854	7	CF551150	AGENCOURT	C 788	14	87.5	982	9	CNS05782	CNS05782
C 716	14	87.5	859	5	BQ889871	AGENCOURT	C 789	14	87.5	986	9	CNS04UDR	CNS04UDR
C 717	14	87.5	859	8	BZ570391	MBH2_1348	C 790	14	87.5	989	2	BE728764	BE728764
C 718	14	87.5	861	3	AY103911	Zee_mays	C 791	14	87.5	990	4	B1410801	B1410801
C 719	14	87.5	862	3	CC708036	OGUGR8TH	C 792	14	87.5	990	5	BQ708919	AGENCOURT
C 720	14	87.5	863	4	BG321590	DB01_01a0	C 793	14	87.5	991	4	CNS05FEA2	CNS05FEA2
C 721	14	87.5	864	1	AU133377	AU133377	C 794	14	87.5	995	4	B1558564	6032405633
C 722	14	87.5	866	6	CD358424	AGENCOURT	C 795	14	87.5	1005	6	CA148958	CA148958
C 723	14	87.5	866	6	CD358424	AGENCOURT	C 796	14	87.5	1005	6	CA148958	CA148958
C 724	14	87.5	867	8	AQ750212	AGENCOURT	C 797	14	87.5	1005	6	CA148958	CA148958
C 725	14	87.5	871	5	BU423977	AGENCOURT	C 798	14	87.5	1012	1	AU090745	AU090745
C 726	14	87.5	871	5	CL102463	AGENCOURT	C 799	14	87.5	1012	9	ECAS43366	ECAS43366
C 727	14	87.5	872	4	BG111391	602281756	C 800	14	87.5	1017	9	CNS05GXP	CNS05GXP
C 728	14	87.5	872	4	BG111391	602281756	C 801	14	87.5	1019	5	BUS20311	BUS20311
C 729	14	87.5	874	9	CK158553	FGAS03982	C 802	14	87.5	1020	5	B0715228	AGENCOURT
C 730	14	87.5	876	9	CC708043	CCUGR88TV	C 803	14	87.5	1030	1	AL557316	AL557316
C 731	14	87.5	879	7	CK159831	FGAS04134	C 804	14	87.5	1033	9	CNS05KIC	CNS05KIC
C 732	14	87.5	881	7	CK156540	FGAS04153	C 805	14	87.5	1034	9	CNS10088	CNS10088
C 733	14	87.5	882	7	CK160000	FGAS04153	C 806	14	87.5	1036	6	CA248169	CA248169
C 734	14	87.5	883	7	CK159412	FGAS04085	C 807	14	87.5	1039	6	CL258403	ZMMBB0616
C 735	14	87.5	885	5	BU141397	603136996	C 808	14	87.5	1045	6	CA789164	AGENCOURT
C 736	14	87.5	886	2	BF185840	601817547	C 809	14	87.5	1052	9	CNS03SVF	AGENCOURT
C 737	14	87.5	887	5	B0710980	AGENCOURT	C 810	14	87.5	1052	9	CNS05EHL	CNS05EHL
C 738	14	87.5	888	4	BM045557	603623701	C 811	14	87.5	1052	9	CNS05EHL	CNS05EHL
C 739	14	87.5	893	7	CNS03258	AGENCOURT	C 812	14	87.5	1054	9	CNS05LJ7	CNS05LJ7
C 740	14	87.5	894	4	B1409472	602961837	C 813	14	87.5	1070	9	CNS0574F	CNS0574F
C 741	14	87.5	895	8	CC412230	PURBEC42TD	C 814	14	87.5	1074	9	CNS04YVI	CNS04YVI
C 742	14	87.5	896	5	CNS04WFB	AL310304	C 815	14	87.5	1076	8	CNS05124	CNS05124
C 743	14	87.5	897	9	CR797873	AGENCOURT	C 816	14	87.5	1078	8	BZ559798	AGENCOURT
C 744	14	87.5	898	7	CK161092	CKI61092	C 817	14	87.5	1082	9	CNS050X	CNS050X
C 745	14	87.5	898	9	CNS05MCO	AL343881	C 818	14	87.5	1082	9	CNS050X	CNS050X
C 746	14	87.5	899	4	B1415002	602991088	C 819	14	87.5	1084	8	CC224467	AGENCOURT
C 747	14	87.5	900	7	CK160354	FGAS04192	C 820	14	87.5	1089	9	CNS05EKS	CNS05EKS
C 748	14	87.5	902	7	CK160334	FGAS04192	C 821	14	87.5	1094	7	CF583772	AGENCOURT
C 749	14	87.5	902	7	CR224767	Forward_B	C 822	14	87.5	1097	9	CNS05CDX	CNS05CDX
C 750	14	87.5	906	5	BQ928686	AGENCOURT	C 823	14	87.5	1099	9	CNS05000	CNS05000
C 751	14	87.5	907	4	BI956538	HYSMEE000	C 824	14	87.5	1101	9	CNS05LPM	CNS05LPM
C 752	14	87.5	907	5	BQ231653	AGENCOURT	C 825	14	87.5	1101	9	CNS05EVE	CNS05EVE
C 753	14	87.5	910	1	AL356370	FGAS04204	C 826	14	87.5	1101	9	CNS05770	CNS05770
C 754	14	87.5	910	7	CK160456	AL356370	C 827	14	87.5	1101	9	CNS059ZN	CNS059ZN

828	14	87.5	1101	9	CNS05T54	AI352705	Tetradon	C 901	13	81.2	215	1	AI565875
829	14	87.5	1106	4	BM801035	BM801035	AGENCOURT	C 902	13	81.2	215	2	BF833898
C 830	14	87.5	1110	5	BO963301	BO963301	AGENCOURT	C 903	13	81.2	215	4	BG842275
831	14	87.5	1121	4	BI730441	BI730441	CG0350765	C 904	13	81.2	215	4	BM447515
832	14	87.5	1123	7	CK162021	CK162021	FGAS01460	C 905	13	81.2	215	8	AZ090935
C 833	14	87.5	1123	7	CK208379	CK208379	FGAS02009	C 906	13	81.2	215	8	AZ097539
C 834	14	87.5	1127	7	BM558565	BM558565	AGENCOURT	C 907	13	81.2	217	8	AZ779530
C 835	14	87.5	1129	8	CC240740	CC240740	CH261-45B	C 908	13	81.2	218	2	BB467859
836	14	87.5	1136	9	CNS0517B	AI316496	Tetradon	C 909	13	81.2	218	6	CA507975
837	14	87.5	1156	4	BM556141	BM556141	AGENCOURT	C 910	13	81.2	218	9	CL209333
838	14	87.5	1164	5	BM908805	BM908805	AGENCOURT	C 911	13	81.2	219	2	BE767980
C 839	14	87.5	1201	4	CNS04VPC	AI309009	Tetradon	C 912	13	81.2	222	9	CE598153
840	14	87.5	1261	5	BQ059904	BQ059904	AGENCOURT	C 913	13	81.2	223	4	BG315747
841	14	87.5	1321	4	BG684874	BG684874	60236608	C 914	13	81.2	223	9	AG588108
842	14	87.5	1354	3	CNS0A5YO	BX823033	Arabidops	C 915	13	81.2	223	9	CE487126
843	14	87.5	1377	3	CNS0A5BP	BX823295	Arabidops	C 916	13	81.2	224	1	AL731948
844	14	87.5	1412	3	CNS0A5FP	AK075586	Mus muscu	C 917	13	81.2	224	9	CE290517
845	14	87.5	1584	3	AK075586	AK075586	Mus muscu	C 918	13	81.2	226	1	AV059982
C 846	14	87.5	1754	4	BG419433	BG419433	602446124	C 919	13	81.2	227	4	BG667885
847	14	87.5	2508	9	AY412901	AY412901	Mus muscu	C 920	13	81.2	230	1	AV258891
848	14	87.5	2928	3	AK046259	AK046259	Mus muscu	C 921	13	81.2	230	5	BO818744
849	14	87.5	3474	3	HSMB00886	AI110229	Homo sapi	C 922	13	81.2	230	9	CE038670
850	14	87.5	3721	3	AK039769	AK039769	Mus muscu	C 923	13	81.2	230	9	CE038670
C 851	14	87.5	4123	3	AK080967	AK080967	Mus muscu	C 924	13	81.2	231	2	BB300495
852	14	87.5	4828	3	HSMB02759	AK791328	Homo sapi	C 925	13	81.2	232	1	AV017466
853	13	81.2	107	8	AZ791730	BX611415	BX611415	C 926	13	81.2	232	2	BB838317
854	13	81.2	111	5	BX611415	AI659777	AI659777	C 927	13	81.2	234	1	AV058652
855	13	81.2	114	1	AL659777	CY150165	Medfct1074	C 928	13	81.2	234	4	AV332448
856	13	81.2	115	7	CV150165	CN636852	139H11_54	C 929	13	81.2	235	9	CE033183
857	13	81.2	117	7	CN636852	BU927050	saa95a101.	C 930	13	81.2	235	9	CE033183
858	13	81.2	118	5	BU927050	BE934180	CWO-HT091	C 931	13	81.2	236	1	AI471018
C 859	13	81.2	120	2	BE934180	CK925050	3FEmgc_01	C 932	13	81.2	236	1	AI841550
C 860	13	81.2	134	7	CK925050	CG656751	OST423872	C 933	13	81.2	238	2	BB037777
C 861	13	81.2	140	9	CG656751	AA855180	aj53b05.8	C 934	13	81.2	238	2	BB037777
C 862	13	81.2	142	1	AA855180	AA426123	zvs2e11.8	C 935	13	81.2	238	2	BB075507
863	13	81.2	145	1	AA426123	AA387643	MRI-ST011	C 936	13	81.2	239	4	BI004928
864	13	81.2	150	2	AA387643	BE171187	QV3-HT054	C 937	13	81.2	240	1	AA072881
C 865	13	81.2	152	2	BE171187	B2767989	SALC_1396	C 938	13	81.2	240	1	AA824455
866	13	81.2	152	8	B2767989	AI842924	UI-M-A01-	C 939	13	81.2	240	5	BX635692
867	13	81.2	153	1	AI842924	BO149076	NP087E09F	C 940	13	81.2	242	6	CB863441
868	13	81.2	155	5	BO149076	AQ005378	CIT-HSP-2	C 941	13	81.2	244	1	AA873831
869	13	81.2	159	8	AQ005378	AI938864	sc61h06.y	C 942	13	81.2	245	1	AV244678
870	13	81.2	163	1	AI938864	AZ717492	RPCI-24-8	C 943	13	81.2	245	8	AZ470216
871	13	81.2	163	8	AZ717492	CE643126	LiGr-G8B-	C 944	13	81.2	246	8	AZ236381
C 872	13	81.2	163	9	CE643126	CB118781	K-RST0165	C 945	13	81.2	247	1	AA706454
873	13	81.2	164	6	CB118781	CM024217	NXRV_037	C 946	13	81.2	247	8	BM841897
C 874	13	81.2	164	6	CM024217	AM387628	MRI-ST011	C 947	13	81.2	248	1	AA831160
C 875	13	81.2	167	9	AM387628	CE074253	LiGr-G8B-	C 948	13	81.2	248	4	BI040623
C 876	13	81.2	177	9	CE074253	CL433016	ZMMBD044	C 949	13	81.2	249	2	AM111813
C 877	13	81.2	180	2	CL433016	BE155402	PML-HT035	C 950	13	81.2	250	1	AV159888
C 878	13	81.2	182	9	BE155402	CL872795	ab685D07.	C 951	13	81.2	251	1	AV348287
C 879	13	81.2	182	9	CL872795	BR115302	7H81a11.x	C 952	13	81.2	251	9	CE334277
C 880	13	81.2	184	2	BR115302	AI893438	mt09h06.x	C 953	13	81.2	252	2	AM462181
881	13	81.2	185	1	AI893438	BF733981	PM2-ANNO9	C 954	13	81.2	252	7	T99612
882	13	81.2	190	2	BF733981	BB248888	BB248888	C 955	13	81.2	253	1	AA226343
C 883	13	81.2	193	2	BB248888	BI424499	gab5D007.	C 956	13	81.2	254	1	AA226343
C 884	13	81.2	193	4	BI424499	T36206	EST98455_Hu	C 957	13	81.2	254	1	AV223233
885	13	81.2	193	7	T36206	BF898513	CM1-WT018	C 958	13	81.2	255	2	AM875451
886	13	81.2	196	2	BF898513	AA163401	me71b09.x	C 959	13	81.2	255	2	AM875451
887	13	81.2	201	1	AA163401	AV104583	AV104583	C 960	13	81.2	257	5	BQ757093
C 888	13	81.2	201	1	AV104583	AM865307	PM4-SNO02	C 961	13	81.2	257	7	CF804443
889	13	81.2	203	2	AM865307	BE207073	ba09h10.y	C 962	13	81.2	258	4	BI053144
C 890	13	81.2	205	2	BE207073	CO133140	EST827811	C 963	13	81.2	259	6	CD037605
891	13	81.2	205	9	CO133140	CG567530	OST193949	C 964	13	81.2	259	9	CR093529
C 892	13	81.2	205	9	CG567530	AV003495	AV003495	C 965	13	81.2	260	1	AA077298
C 893	13	81.2	208	1	AV003495	CG605628	OST282556	C 966	13	81.2	261	1	AV033563
C 894	13	81.2	209	9	CG605628	AV243769	AV243769	C 967	13	81.2	264	4	BM099980
C 895	13	81.2	211	1	AV243769	AV282192	AV282192	C 968	13	81.2	267	4	BM818153
C 896	13	81.2	211	8	AV282192	AQ288623	rbdb0033C	C 969	13	81.2	268	2	AM012658
C 897	13	81.2	213	1	AQ288623	AI845009	UT-M-BG0-	C 970	13	81.2	268	2	AM012658
898	13	81.2	213	1	AI845009	AA352555	EST60648	C 971	13	81.2	269	2	AM518921
899	13	81.2	214	1	AA352555	CD271311	TI43A0028	C 972	13	81.2	269	2	BB318197
900	13	81.2	214	6	CD271311	AI566875	tq49g06.x	C 973	13	81.2	269	2	BB318197

C 974	13	81.2	259	7	CR766135	CR766135	DKFZP4459F
C 975	13	81.2	272	1	AA281608	AA281608	ztc03a07.8
C 976	13	81.2	272	9	CR067653	CR067653	Forward.b
C 977	13	81.2	272	9	CL212215	CL212215	G034C09 G
C 978	13	81.2	273	1	AA358138	AA358138	EST66978
C 979	13	81.2	273	2	BB398396	BB398396	BB398396
C 980	13	81.2	273	2	BB516752	BB516752	BB516752
C 981	13	81.2	273	2	BB838456	BB838456	BB838456
C 982	13	81.2	273	2	BB320608	BB320608	NF035A02R
C 983	13	81.2	274	7	CK365998	CK365998	C0287B05-
C 984	13	81.2	276	2	AW149154	AW149154	xfl6b12.x
C 985	13	81.2	277	1	AA678613	AA678613	ab03c06.8
C 986	13	81.2	278	2	BB570252	BB570252	BB570252
C 987	13	81.2	278	2	BB716658	BB716658	BB716658
C 988	13	81.2	279	1	A1548658	A1548658	UI-R-C3-t
C 989	13	81.2	279	2	AW530595	AW530595	UI-R-C4-a
C 990	13	81.2	279	2	BB041570	BB041570	BB041570
C 991	13	81.2	279	7	CN682470	CN682470	E0164H11-
C 992	13	81.2	280	2	BB307690	BB307690	BB307690
C 993	13	81.2	280	2	BB521626	BB521626	BB521626
C 994	13	81.2	281	1	A1857722	A1857722	w121a04.x
C 995	13	81.2	281	2	BB195358	BB195358	BB195358
C 996	13	81.2	282	1	AA341503	AA341503	EST46928
C 997	13	81.2	283	1	AV125965	AV125965	AV125965
C 998	13	81.2	284	1	A1041147	A1041147	ov69f04.x
C 999	13	81.2	284	9	AG212719	AG212719	Oryza sat
C 1000	13	81.2	284	9	BX946334	BX946334	Arabidops

ALIGNMENTS

CR61155	DKR204559
AA281568	ztc3077.8
CR067663	Forward B
CL212123	G04C09 G
AA358118	ESY66798
BB338336	B5136792
BB167572	B5116752
BB384546	BB338456
BB330608	NF0355005
CC316998	C0287005
AW119154	xlf6b1.2
BB570252	B5570252
BB570252	B5570252
BB16658	BB116558
AA134658	U1-R-03-
BB041570	U1-R-04-
AA041570	B041570
CN682470	E0164111
BB307660	BB307660
BB521626	BB521626
AA158772	w121a04.5
BB158772	BB158772
AA431565	ESY46628
AA125503	AA125503
AA1641147	ov69f04.x.x
AG212719	Oryza sativa
AX946634	Arabidopsis

ORIGIN

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="BN0148"
/name="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORNSTIS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

QY 1 AAAGCCACCCAAAGGCA 16
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Db 16 AAAGCCACCCAAAGGCA 31

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
B1049449	B1049449	396 bp mRNA, linear	CM2-GN0295-020101-655-a07	GN0295	Homo sapiens CDNA, mRNA sequence.	Homo sapiens	Homo sapiens (human)
			B1049449	B1049449.1	GI:14456979	EST.	

[illegible]

REFERENCE	AUTHORS
1 (bases 1 to 396)	Dias Neto, E., Garcia Correa, R., Veijovskí-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20020263
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01505-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

FEATURES

FEATURES	Location/Qualifiers
source	1. .384
	/organism="Homo sapiens"

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/cloze_lib="cN00295"
/ncbi-organ: placenta:normal: Vector: puc18: Site:1:
Smat, Site:2: Smat, A mini-library was made by cloning
products derived from ORSTS PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were

```

ORIGIN performed under low stringency conditions."

Query Match 100.0%; Score 16; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
|||||
Db 148 AAAGCCACCCAGGCA 163

RESULT 3
CE327035 441 bp DNA linear GSS 26-SEP-2003
LOCUS tigr-g88-dog-17000333941473 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
CE327035
VERSION CE327035.1 GI:36139166
KEYWORDS GSS.
SOURCE
ORGANISM Canis familiaris (dog)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 441)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis

TITLE
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 148175432
PubMed 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.

FEATURES

source
Location/Qualifiers
1..441
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BclXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
|||||
Db 73 AAAGCCACCCAGGCA 88

RESULT 4
AA103554 464 bp mRNA linear EST 29-OCT-1996
LOCUS mol24110.1 life Tech mouse embryo 13 5dpc 10666014 Mus musculus
DEFINITION cDNA clone IMAGE:554563 5', mRNA sequence.
AA103554
VERSION AA103554.1 GI:1649714
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 464)

AUTHORS

Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepcie, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL The WashU-HMI Mouse EST Project
COMMENT Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:335355

Putative full length read
vector to vector length is 510
Seq primer: -28M13 rev1 from Amersham.
Location/Qualifiers

FEATURES

source
1..464
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="IMAGE:554563"
/tissue_type="embryo"
/dev_stage="13.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
/note="Organ: whole embryo; Vector: PCMV-SPORT2; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 13.5dpc embryos. PCMV-SPORT2 vector."

ORIGIN

Query Match 100.0%; Score 16; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
|||||
Db 275 AAAGCCACCCAGGCA 260

RESULT 5

BE144757 496 bp mRNA linear EST 21-JUN-2000
LOCUS CM0-HT0180-041099-065-c06 HT0180 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE144757
ACCESSION BE144757
VERSION BE144757.1 GI:8607481
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 496)
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripte/gethtml2.pl?tl=et2-CM0-HR0180-041>)
 099-065-006&t3=1999-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 496.

FEATURES

Source

Location/Qualifiers
 1..496
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="HR0180"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAGCCACCCAGGCA 16
 |||||
 229 AAAGCCACCCAGGCA 244

RESULT 6
 LOCUS CF755881 587 bp mRNA linear EST 17-OCT-2003

DEFINITION DAPF1.2 A12.b1 A011 Drought-stressed after flowering Sorghum
 bicolor cDNA clone DAPF1.2_A12_A011 5', mRNA sequence.
 CF755881
 CF755881.1 GI:37704961

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Sorghum bicolor (sorghum)
 Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 587)
 Cordonnier-Pratt, M.-M., Zhang, D., McCartor, K., Nguyen, H.T. and
 Pratt, L.H.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 An EST Database from Sorghum: Subtracted post-flowering drought
 stressed leaf tissues
 Unpublished (2003)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@uga.edu

Library constructed at Texas Tech University by Denshi Zhang and
 Jianhang Jia in the laboratory of Dr. Henry Nguyen. Sequencing was
 done in the laboratory for Genomics and Bioinformatics, University
 of Georgia. Sequence ends have been trimmed to exclude vector and
 regions below phred quality 16. Three-prime sequences are presented
 as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: JENNEV (CAGGAACGCTATGACC).

FEATURES

Source

Location/Qualifiers
 1..587
 /organism="Sorghum bicolor"
 /mol_type="RNA"
 /cultivar="B35"
 /db_xref="taxon:4558"

/clone="DAPF1.2 A12 A011"
 /dev_stage="Post-flowering"
 /lab_host="Electromax DH10B (BRL)"
 /clone_lib="Drought-stressed after flowering"
 /note="Organ: Leaf; Vector: pBluescriptSK-; Site 1: XhoI;
 Site 2: EcoRI; The library was prepared from polyA+ RNA
 from leaves harvested from post-flowering,
 drought-stressed Sorghum bicolor cv. B35. Double-stranded
 cDNA was cloned unidirectionally using the Unizap system
 from Stratagene. After amplification, the library was
 subtracted by re-association hybridization. Inserts can be
 excised with XhoI and EcoRI."

ORIGIN

Query Match 100.0%; Score 16; DB 7; Length 587;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAGCCACCCAGGCA 16
 |||||
 225 AAAGCCACCCAGGCA 240

RESULT 7
 LOCUS BQ385327/c 623 bp mRNA linear EST 22-MAY-2002

DEFINITION NISC.mn11f10.v1 NICH.D.XGC_Ov1 Xenopus laevis cDNA clone
 IMAGE:5073186 5', mRNA sequence.
 BQ385327
 BQ385327.1 GI:21073014
 EST.
 Xenopus laevis (African clawed frog)
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 623)
 NIH-XGC <http://image.llnl.gov/image/html/xenopus1b.info.shtml>.
 National Institute of Child Health and Human Development, National
 Cancer Institute, Xenopus Gene Collection
 Unpublished (2002)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 CDNA Library Preparation:
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@image.llnl.gov
 Plate: LLAM1196 row: L column: 19
 Seq primer: M13R1 reverse primer (ABT).

FEATURES

Source

Location/Qualifiers
 1..623
 /organism="Xenopus laevis"
 /mol_type="RNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:5073186"
 /sex="female"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICH.D.XGC_Ov1"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NciI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.0 kb. Constructed by Life
 Technologies."

ORIGIN

Query Match 100.0%; Score 16; DB 5; Length 623;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAGCCACCCAGGCA 16
 |||||

was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PhC I."

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCAGGCA 16
|||||
DB 434 AAAGCACCAGGCA 419

RESULT 10 666 bp mRNA linear EST 23-SEP-2003
CA083440
LOCUS SCEPAM013G09.g AM2 Saccharum officinarum cDNA clone SCEPAM013G09
DEFINITION
5', mRNA sequence.
CA083440
VERSION CA083440.1 GI:34936751
KEYWORDS
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 666)
Vector: A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcap.unesp.br
Plate: 013 row: G column: 09
Seq primer: T7 Promoter Primer.

FEATURES

source

Location/Qualifiers
1..666
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEPAM013G09"
/lab_host="DH10B"
/clone_id="AM2"
/note="Organ: Apical meristem and tissues surrounding of
immature plants; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of immature
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a Sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCAGGCA 16
|||||
DB 471 AAAGCACCAGGCA 486

RESULT 11
AV359761/c

LOCUS

AV359761 RIKEN full-length enriched, adult male eyeball Mus
musculus cDNA clone 7530401G06 3', mRNA sequence.

ACCESSION

AV359761

VERSION

AV359761.2 GI:16397410

KEYWORDS

EST.
Mus musculus (house mouse)

SOURCE

Mus musculus

Mus musculus

REFERENCE

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Nov 13, 1999 this sequence version replaced gi:6406899.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9226
Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source

Location/Qualifiers
1..700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7530401G06"
/sex="male"
/tissue_type="eyeball"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, adult male
eyeball"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTATTAATTAATCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"

ORIGIN

Query Match 100.0%; Score 16; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 110 AAAGCCACCCAGGCA 95

RESULT 12
CD778583/c 770 bp mRNA linear EST 01-JUL-2004
LOCUS EST649944 RAA Rhipicephalus appendiculatus cDNA clone RAAA309 3'
DEFINITION end, mRNA sequence.

ACCESSION CD778583
VERSION CD778583.1 GI:49534256
KEYWORDS EST.
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus

REFERENCE Eukaryote, Metazoa, Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
1 (bases 1 to 770)
Nene, V., Lee, Y., Skilton, R., Mwaura, S., Quackenbush, J., Gardner, M. and Bishop, R.

TITLE An index of genes transcribed in the salivary glands of Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST649945
Contact: Vithvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org

FEATURES
Source
1. .770
Location/Qualifiers

1. .770
Location/Qualifiers

/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAAA309"
/dev_stage="Adult"
/lab_host="B. coli strain DH10B-Tona"
/clone_id="RAA"
/note="Organ: Salivary glands; Vector: pCMVSPORT6.0.cdb; Salivary glands were dissected on day four after initiation of feeding. Total RNA was prepared using acid guanidium thiocyanate-phenol-chloroform extraction. The cDNA library was custom prepared by Invitrogen Corporation. Briefly, first strand cDNA was primed using oligo(dT) containing a NotI site. Size fractionated double

ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 257 AAAGCCACCCAGGCA 242

RESULT 13
BI250824 895 bp mRNA linear EST 17-JUL-2001
LOCUS 602993448F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149306 5'
DEFINITION mRNA sequence.

ACCESSION BI250824
VERSION BI250824.1 GI:14799568
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 895)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM1368 row: p column: 11
High quality sequence start: 4
High quality sequence stop: 741.
Location/Qualifiers

1. .895
Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5149306"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN

Query Match 100.0%; Score 16; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 2 AAAGCCACCCAGGCA 17

RESULT 14
CA474404 975 bp mRNA linear EST 12-NOV-2002
LOCUS CA474404/c
DEFINITION AGENCOURT_10667749 NCI_CGAP_ZK1d1 Danio rerio cDNA clone

IMAGE:6795444.5', mRNA sequence.
 CA474404
 VERSION CA474404.1 GI:24930756
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 975)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Leonard I. Zon, M.D.
 CDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LLM14305 row: 1 column: 11
 High quality sequence stop: 314.
 Location/Qualifiers
 1..975
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:6795444"
 /lab_host="DH10B (T1-resistant)"
 /note="Organ: kidney; Vector: PCW-Sports.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI CGAP library."

ORIGIN
 Query Match 100.0%; Score 16; DB 6; Length 975;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 621 AAAGCCACCCAGGCA 606

RESULT 15
 W34362/c
 LOCUS
 DEFINITION 987 bp mRNA linear EST 11-SEP-1996
 IMAGE:31815.5', similar to SW:KELC_DROME Q04652 RING CANAL PROTEIN
 ; mRNA sequence.
 W34362
 W34362.1 GI:1316273
 EST.
 Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 987)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Scheibenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 CONTACT: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:209431
 Seq primer: ETP-Primer
 High quality sequence stop: 363.
 Location/Qualifiers
 1..987
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:31815.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares mouse p3NMF19.5"
 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

ORIGIN
 Query Match 100.0%; Score 16; DB 7; Length 987;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 361 AAAGCCACCCAGGCA 346

RESULT 16
 CG754259/c
 LOCUS
 DEFINITION 1684 bp DNA linear GSS 24-OCT-2003
 P049-3-E10-ya Ppa EcoRI BAC library Pristionchus pacificus genomic,
 genomic survey sequence.
 CG754259
 CG754259.1 GI:37979569
 GSS.
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasterida; Pristionchus.
 1 (bases 1 to 1684)
 Srinivasan, J., Sins, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
 An integrated physical and genetic map of the nematode Pristionchus pacificus
 Mol. Genet. Genomics 269 (5), 715-722 (2003)
 22835951
 12884007
 CONTACT: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 Class: BAC ends.
 Location/Qualifiers
 1..1684
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"

FEATURES
 source

RESULT 18
AK078669/c
LOCUS
DEFINITION
AK078669 2368 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male eyeball cDNA, RIKEN full-length enriched library, clone:7530401G06 product:CDNA FLJ32015 FIS, CLONE NTONG1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS K14C RELATED PROTEIN 1 homolog (Homo sapiens), full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK078669.1 GI:26098028
Mus musculus (house mouse)
HTC; CAP trapper.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636
2
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2368)
Aaach, J., Aizawa, K., Akinura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazaki, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, K., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyu, T., Yasunishi, A., Yamamatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
source
1..2368
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:7530401G06"
/db_xref="taxon:10090"
/clone="7530401G06"
/sex="male"
/tissue_type="eyeball"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
83..1949
/note="CDNA FLJ32015 FIS, CLONE NTONG1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS K14C RELATED PROTEIN 1 homolog (Homo sapiens) (SPTK106MR2, evidence: PASTY, 91.5%ID, 93.8%length, match=1329)
putative"
2347..2352
/note="putative"
2368
/note="putative"

misc_feature
polya_signal
polya_site
ORIGIN
Query Match 100.0%; Score 16; DB 3; Length 2368;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 AAAGCCACCACCAAGCA 16
|||||
Db 1778 AAGGCCACCCCAAGCA 1763

RESULT 19
BB198017
LOCUS
DEFINITION
BB198017 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330105M01.3', mRNA sequence.
VERSION
ACCESSION
BB198017
BB198017.1 GI:8862970
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 231)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Tagawa, A., Takahashi, F., Tomimaga, N., Toyu, T., Tsunoda, Y., Watanabe, S., Yamamatsu, T., Yamamatsu, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
 Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Thermolabile and thermostable enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, U., Shibata, K., Iwata, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y., and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.
 Location/Qualifiers
 1. 231
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A330105M01"
 /sex="male"
 /tissue_type="spinal cord"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="RIKEN full-length enriched, adult male spinal
 cord"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATTCGAGTTATTAATTAATTCCTCCCTCCCTCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified Bluescript KS(+) after bulk excision from lambda
 FLC I."

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAGCACCACCAAGGC 15
 |||||
 Db 138 AAAGCACCACCAAGGC 152

RESULT 20
 BF924007 268 bp mRNA linear EST 19-JAN-2001
 LOCUS CM2-NT0170-251100-530-h08 NT0170 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF924007
 VERSION BF924007.1 GI:12319895
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 268)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL 20202663
 MEDLINE 10737800
 PUBMED
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t=CM2-NT0170-251100-530-h08&t3=2000-11-25&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 268.
 Location/Qualifiers
 1. 268
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1lb="NT0170"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

FEATURES

source

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 AAGCACCACCAAGCA 16
 |||||
 Db 84 AAGCACCACCAAGCA 98

RESULT 21
 BB090939 285 bp mRNA linear EST 23-JUN-2000
 LOCUS BB090939 RIKEN full-length enriched, 12 days embryo, embryonic body
 DEFINITION between diaphragm region and neck Mus musculus cDNA clone
 9430028F19 3', mRNA sequence.
 ACCESSION BB090939
 VERSION BB090939.1 GI:8674186
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 285)
 Kono, H., Alizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
 Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, D., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
 Kusakabe, M., Matsuyama, T., Miki, R., Miuno, Y., Nakamura, M., Oda, H.,
 Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
 Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shitaki, T.,
 Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
 Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Wataniki, A.,

modified pBluescript KS(+) after bulk excision from lambda
FLC 1."

Query Match 93.8%; Score 15; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
DB 169 AAAGCCACCCAGGC 155

RESULT 23
W40391
LOCUS 294 bp mRNA linear EST 20-MAY-1996
DEFINITION z880e10.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328650 5' similar to gb:D13748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN); mRNA sequence.

ACCESSION W40391.1 GI:1324172
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 294)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Warr, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 243.

FEATURES
source
Location/Qualifiers
1..294

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1262854"
/db_xref="taxon:9606"
/clone="IMAGE:328650"
/issue_type="pancreatic islet"
/lab_host="SOX cells (kanamycin resistant)"
/clone_lib="Pancreatic Islet"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993) Takeda et al. Cloned unidirectionally. Primer: Oligo dt. -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequencé: 5' CTCGAGTTT TTT TTT TTT TTT TTT TTT 3'"

ORIGIN
Query Match 93.8%; Score 15; DB 7; Length 294;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
DB 209 AAAGCCACCCAGGC 223

RESULT 24

BI036238
LOCUS 306 bp mRNA linear EST 14-JUN-2001

DEFINITION CM3-NT0245-030101-599-f10 NT0245 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI036238
VERSION BI036238.1 GI:14442864
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 306)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM3&l2=CM3-NT0245-030101-599-f10&l3=2001-01-03&l4=1)

Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 306.

FEATURES
source
Location/Qualifiers
1..306

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="NT0245"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 93.8%; Score 15; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
DB 113 AAGCCACCCAGGCA 127

RESULT 25
BB251202
LOCUS 310 bp mRNA linear EST 06-JUN-2000
DEFINITION BB251202 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730045D02 3', mRNA sequence.

ACCESSION BB251202
VERSION BB251202.1 GI:8943948
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

JOURNAL Unpublished (1998)
 COMMENT Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org

FEATURES
 Source
 1. .328
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="RG1H086"
 /tissue_type="mix - brain, ovary, placenta, kidney, lung, liver, embryo, heart, muscle, spleen"
 /lab_host="SOLR"
 /clone_lib="Rat gene index, normalized rat, norvegicus, Bento Soares"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Estimated insert size approx.1 kb"

Query Match 93.8%; Score 15; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGC 15
 |||||
 243 AAGCCACCCAGGC 257

RESULT 28
 LOCUS BF935524 362 bp mRNA linear EST 22-JAN-2001
 DEFINITION IL2-NT0203-271200-322-A10 NT0203 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF935524
 VERSION BF935524.1 GI:12352848
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 362)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negat, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

FEATURES
 This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0203-271200-322-A10&t3=2000-12-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 324.
 Location/Qualifiers

source

1. .362
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0203"
 /note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 93.8%; Score 15; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
 |||||
 184 AAGCCACCCAGGCA 198

RESULT 29
 LOCUS CV001930 365 bp mRNA linear EST 18-AUG-2004
 DEFINITION csa02-2m63-g01 Csa02 Cucumis sativus cDNA clone csa02-2m63-g01 5', mRNA sequence.
 ACCESSION CV001930
 VERSION CV001930.1 GI:51361153
 KEYWORDS EST.
 SOURCE Cucumis sativus (cucumber)
 ORGANISM Cucumis sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 1 (bases 1 to 365)
 dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P., Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M., Leebens-Mack, J., Landherr, L., Perl-Treves, R., Ilut, D. and Wall, K.

TITLE Generation of ESTs from early female flower buds of Cucumis sativus
 JOURNAL Unpublished (2003)
 COMMENT Contact: Claude dePamphilis or James Leebens-Mack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwt3@psu.edu or jh110@psu.edu
 The sequence provided is trimmed of vector and low quality regions. Full sequence and original trace file are available from the Plant Genome Network website (http://pgn.cornell.edu)
 Plate: csa02-2m63 row: 9 column: 01
 Seq primer: M13P.

FEATURES
 source

1. .365
 /organism="Cucumis sativus"
 /mol_type="mRNA"
 /db_xref="taxon:3659"
 /clone="csa02-2m63-g01"
 /tissue_type="female flower buds"
 /dev_stage="clmm buds"
 /lab_host="SOLR"
 /clone_lib="Csa02"
 /note="Vector: pBluescript SK (+/-); Site_1: EcoRI; Site_2: XhoI; This is a directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at http://fgp.bio.psu.edu"

ORIGIN

Query Match 93.8%; Score 15; DB 7; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 DB 239 AAAGCCACCCAGGC 253

RESULT 30

LOCUS CB691996 375 bp mRNA linear EST 10-APR-2003
 DEFINITION AMGNMNC:SRPG2-00067-E11-A SRPG2 (10238) Rattus norvegicus cDNA
 clone SRPG2-00067-e11 5', mRNA sequence.

ACCESSION CB691996
 VERSION CB691996.1 GI:29749143
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine;

REFERENCE 1 (bases 1 to 375)
 AUTHORS Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00067 row: e column: 11.
 Location/Qualifiers

FEATURES

source 1..375
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="srpg2-00067-e11"
 /tissue_type="penal gland brain"
 /clone_lib="srpg2 (10238)"
 /note="Vector: pSPORT1, Site_1: SalI; Site_2: NotI; penal
 gland brain region"

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 DB 343 AAAGCCACCCAGGC 357

RESULT 31

LOCUS CE698527 394 bp DNA linear GSS 29-SEP-2003
 DEFINITION tigr-gss-dog-17000368753766 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CE698527
 VERSION CE698527.1 GI:37017751
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 394)
 AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)

TITLE JOURNAL
 MEDLINE 22875432

PUBMED

14512627
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers

FEATURES

source 1..394
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 93.8%; Score 15; DB 9; Length 394;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 DB 103 AAAGCCACCCAGGC 89

RESULT 32

LOCUS CE047936 401 bp DNA linear GSS 24-SEP-2003
 DEFINITION tigr-gss-dog-17000357497477 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CE047936
 VERSION CE047936.1 GI:35087093
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 401)
 AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)

TITLE JOURNAL
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers

FEATURES

source 1..401
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 93.8%; Score 15; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGCCACCCAGGCA 16

Db 238 AAGCCACCAAGCA 224

RESULT 33
BIS56031 408 bp mRNA linear EST 30-AUG-2001

DEFINITION
350188 MRC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION
BIS56031

VERSION
BIS56031.1 GI:15377141

KEYWORDS
EST.

SOURCE
Bos taurus (cow)

ORGANISM
Bos taurus
Bos taurus
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 (bases 1 to 408)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Cabaas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pette,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
Genome Res. 11 (4), 626-630 (2001)

JOURNAL
21180013

MEDLINE
11282978

COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGATCGACG
Plate: 114 row: C column: 7
Seq primer: ATTAGGTGACCTATAG.
Location/Qualifiers
1. .408
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from day 20 and day 40
embryos."

FEATURES
Source

ORIGIN

Query Match 93.8%; Score 15; DB 4; Length 408;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 AAGCCACCAAGCA 16
|||||
74 AAGCCACCAAGCA 88

Db 74 AAGCCACCAAGCA 88

RESULT 34
AA053186 417 bp mRNA linear EST 13-SEP-1996
LOCUS
DEFINITION
2172a04.c1 StrataGene colon (#937204) Homo sapiens cDNA clone
IMAGE:510126 5' similar to gb:DJ1748 EUKARYOTIC INITIATION FACTOR
4A-I (HUMAN);, mRNA sequence.

ACCESSION
AA053186
AA053186.1 GI:1544395

VERSION
EST.

KEYWORDS
Homo sapiens (human)

SOURCE

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 417)
Hiller,L., Lennon,G., Becker,M., Ronaldo,M.F., Chipelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevisan,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.

TITLE
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

JOURNAL
97044478

MEDLINE
8889549

COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28M13 rev2 from AmerSham
High quality sequence stop: 404.
Location/Qualifiers
1. .417
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3813459"
/db_xref="taxon:9606"
/clone="IMAGE:510126"
/tissue_type="tumor"
/cell_line="T84 carcinoma cell line"
/lab_host="SOLR cells (Karamycin resistant)"
/clone_id="Stratagene colon (#937204)"
/note="Organ: colon; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGCGACG 3' -3' adaptor sequence: 5'
CTCAGCTTTTCTTTTCTTTT 3' "

FEATURES
Source

ORIGIN

Query Match 93.8%; Score 15; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AAGCCACCAAGGC 15
|||||
289 AAGCCACCAAGGC 303

Db 289 AAGCCACCAAGGC 303

RESULT 35
B0198462 419 bp mRNA linear EST 07-MAY-2003
LOCUS
DEFINITION
NKLIV31.B01.F NKLIV (Nef Xylem late wood Vertical) Pinus taeda cDNA
clone NKLIV31.B01.5' similar to Arabidopsis thaliana sequence
AT5G47030 ATP synthase delta chain, mitochondrial precursor
(sp|O96252) see <http://mips.gsf.de/proj/thal/db/index.html>, mRNA
sequence.

ACCESSION
B0198462
B0198462.1 GI:20384424

VERSION
EST.

KEYWORDS
Pinus taeda (loblolly pine)

SOURCE
Pinus taeda

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Sederoff,R.
1 (bases 1 to 419)

REFERENCE
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)

TITLE
JOURNAL

COMMENT
Contact: Sederoff, Ron

FEATURES

Location/Qualifiers

ORIGIN

QY 1 AAAGCCACCCCAAGGC 15
|||||
Db 246 AAAGCCACCCCAAGGC 232

ACCESSION	AA147417	
VERSION	AA147417.1	GI:1716788
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

TITLE
JOURNAL
Generation and analysis of 250,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
MEDLINE
57044478

COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available royalty-free through LINTL; contact the
IMAB Consortium (info@imab.ljlnl.gov) for further information.
Insert Length: 1549 Std Error: 0.00

FEATURES
SOURCE

ORIGIN

	QY	1	AAAGCCACCCAAGGC	15
	Db	284	AAAGCCACCCAAGGC	298

ACCESSION	CN125873
VERSION	CN125873.1
KEYWORDS	GI:45950664
SOURCE	EST.
ORGANISM	Sorghum bicolor (sorghum)

COMMENT

Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: immpact@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.

FEATURES

Source

```

"organism":"Scorinnum bicolor"
"mol_type":"mrna"
"cultivar":"Brx623"
"db_xref":"taxon:44588"
"clone":"RH01-3 G11 A002"
"lab_host":"DH10B-T1 phage-resistant E. coli"
"note_1b":"acid and alkaline treated roots"
"note_1c":"pHE18-FM3, sites_1: XhoI,
"note_1d":"Organ. Root. Vector: pHE18-FM3, sites_1: XhoI,

```

Site 2: XhoI; The library was prepared from polyA+ RNA from 8-day-old roots harvested from Btx623 sorghum seedlings grown in hydroponic culture. HCl was added to a pH of 3.0 to some seedlings, KOH to a pH of 9.0 for others. Roots were harvested 3, 12 and 27 hr after addition and pooled for RNA preparation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGCTG, 3-prime DraIII site is CACCAGTGT). XhoI excises the cDNA insert."

ORIGIN

Query Match 93.8%; Score 15; DB 7; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
|||||
Db 193 AAGCCACCCAGGCA 207

RESULT 38 455 bp mRNA linear EST 27-DEC-2002
CA902085 PCS04956 scarlet Runner Bean Suspensor Region Triplex2 Phaseolus
LOCUS coccineus cDNA 5' similar to Nucleoid DNA-binding protein, mRNA
DEFINITION

ACCESSION CA902085 GI:27389077
VERSION EST.
KEYWORDS Phaseolus coccineus
SOURCE Phaseolus coccineus
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
1 (bases 1 to 455)
Bui,A.O., Le,B.H., Weterings,K., Bi,Y.-P., Choi,D.-S.,
McElroy,K.E., Choi,P.S., Harada,J.U., Fischer,R.L. and
Goldberg,R.B.
Gene Activity in Different Regions of a Post-Fertilization Plant
Embryo by EST Analysis
Unpublished (2002)
Contact: Goldberg, R.B.
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Seq primer: 5' Triplex
POLYA=No.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1..455
/organism="Phaseolus coccineus"
/mol_type="mRNA"
/cultivar="Hammond's Dwarf Scarlet"
/db_xref="taxon:3886"
/dev_stage="6-days post-pollination"
/clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
/note="Organ: Suspensor Region of Globular-stage Embryos;
Vector: Triplex2; Site 1: SfiI; Site 2: SfiI; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
[Weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the SfiI restriction site
of the lambda Triplex2 vector (Clontech), and the
recombinant cDNAs were transformed into E. coli XL1-Blue
cells (Clontech). Suspensor cDNA plasmids used for
directional sequencing were obtained by in vivo excision

from the lambda Triplex2 recombinants in E. coli BM25.8
cells (Clontech)."

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
|||||
Db 201 AAGCCACCCAGGCA 215

RESULT 39 459 bp mRNA linear EST 27-JAN-1997
AA205003
LOCUS
DEFINITION zg72e12.r1 Stragatene neuroepithelium (#937231) Homo sapiens cDNA
clone IMAGE:647182 5' similar to gb:DJ3748 EUKARYOTIC INITIATION
FACTOR 4A-1 (HUMAN); mRNA sequence.
AA205003
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 459)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B.,
Chisoso,S., Dietrich,N., Dubuque,T., Favello,A., Gish,M.,
Hawkins,M., Hultman,M., Kucada,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Scheilenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasaki,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 326.

FEATURES

source

Location/Qualifiers
1..459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5217434"
/db_xref="taxon:9606"
/clone="IMAGE:647182"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stragatene neuroepithelium (#937231)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2
cells (Ntera-2/cl.D) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATCGGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN

Query Match 93.8%; Score 15; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 15
|||||
Db 285 AAGCCACCCAGGCA 299

